

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model
Run on: March 8, 2005, 20:45:19 ; Search time 360 Seconds
(without alignments)
5820.744 Million cell updates/sec

Title: US-09-774-490-1
Perfect score: 4896
Sequence: 1 aatctttatttctgatg.....aggcttttttcttaataacc 2709

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2.1/USPTO.spool.p/US09774490/runat_08032005.140757.14830/app_query.fasta_1.2887
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOLOCAL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09774490 @CNC 1.1.407 @runat_08032005.140757.14830 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	2	AAR71380 Human sem
2	4201	85.8	771	4	AA662726 Amino aci
3	4201	85.8	771	5	AB956413 Human ova
4	4201	85.8	771	7	ADD08934 Human sem
5	4201	85.8	771	7	ADE25760 Human pro
6	4201	85.8	771	8	ADQ19751 Human sof
7	4197	85.7	770	7	ADN95333 Human BFC
8	4194	85.7	796	2	AA121264 Human sem
9	2562	52.3	477	2	AAR74175 Human col
10	2245.5	45.9	777	2	AAY27127 Human bra

11	2245.5	45.9	777	3	AA999427 Human PRO
12	2245.5	45.9	777	4	AA666176 Protein o
13	2245.5	45.9	777	4	AAU29197 Human PRO
14	2245.5	45.9	777	6	ABU58573 Human PRO
15	2245.5	45.9	777	6	ABU88121 Novel hum
16	2245.5	45.9	777	6	ABU84436 Human sec
17	2245.5	45.9	777	6	ABR66310 Human sec
18	2245.5	45.9	777	6	ABR65700 Human sec
19	2245.5	45.9	777	6	ABU99640 Human sec
20	2245.5	45.9	777	6	ABU82879 Human PRO
21	2245.5	45.9	777	6	ABU90000 Novel hum
22	2245.5	45.9	777	6	ABR68249 Human sec
23	2245.5	45.9	777	6	ABU96302 Novel hum
24	2245.5	45.9	777	6	ABU92733 Human sec
25	2245.5	45.9	777	6	ABO08810 Human sec
26	2245.5	45.9	777	6	ABO02862 Human sec
27	2245.5	45.9	777	6	ABR75016 Human sec
28	2245.5	45.9	777	6	ABR94778 Human sec
29	2245.5	45.9	777	6	ABU85751 Human PRO
30	2245.5	45.9	777	6	ABU98911 Novel hum
31	2245.5	45.9	777	6	ABU98126 Novel hum
32	2245.5	45.9	777	6	ABU91832 Novel hum
33	2245.5	45.9	777	6	ABU89525 Human PRO
34	2245.5	45.9	777	6	ABU86366 Human sec
35	2245.5	45.9	777	6	ABU67579 Human sec
36	2245.5	45.9	777	6	ABU80607 Human PRO
37	2245.5	45.9	777	6	ABR99525 Human sec
38	2245.5	45.9	777	6	ABR98915 Human sec
39	2245.5	45.9	777	6	ABO16438 Human sec
40	2245.5	45.9	777	6	ABR92338 Human sec
41	2245.5	45.9	777	6	ABO18979 Human sec
42	2245.5	45.9	777	6	ABR78400 Human sec
43	2245.5	45.9	777	6	ABU85136 Novel hum
44	2245.5	45.9	777	6	ABO00275 Novel hum
45	2245.5	45.9	777	6	ABO11607 Human sec

ALIGNMENTS

RESULT 1
AAR71380
ID AAR71380 standard; protein; 771 AA.
XX AC AAR71380;

XX AC
XX AC
DT 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX AC
DE Human semaphorin III protein.

XX AC
KW Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium;
KW variola major virus; smallpox; semaphorin receptor binding activity;
KW modulation; nerve cell growth; immune response; viral pathogenesis;
KW neurological disease; neuro-regeneration; oncological infection.

XX OS Homo sapiens.

XX PN WO9507706-A1.

XX PD 23-MAR-1995.

XX PF 13-SEP-1994; 94WO-US010151.

XX PR 13-SEP-1993; 93US-00121713.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Goodman CS, Kolodkin AL, Matthes D, Bentley DR, O'Connor T;

XX DR WPI, 1995-131177/17.

XX DR N-PSDB; AAQ87442.

XX PT New class of semaphorin peptide(s) and polypeptide(s) - are potent

modulators of nerve cell growth and regeneration.
 Example 2; Page 60-63; 101pp; English.

The sequence of the human semaphorin III protein. The proteins encoded by the grasshopper semaphorin I (AA087441), human semaphorin III, vaccinia virus semaphorin IV (AA087443), Drosophila semaphorin I and II (AA087444-5), Tribolium semaphorin I (AA087446) or variola major (smallpox) virus semaphorin IV (AA087447) genes were used to generate a series of peptides (AA0870370-R70418), which retain semaphorin receptor binding activity. The semaphorin derived or semaphorin receptor derived peptides are potent modulators of nerve cell growth, immune responsiveness and viral pathogenesis. They can be used in diagnosis and treatment of neurological disease and neuro-regeneration, immune modulation and diagnosis and treatment of viral and oncological infection and diseases. (Updated on 25 -MAR-2003 to correct PN field.)

Sequence 771 AA;

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 2 Gaps: 0

US-09-774-490-1 (1-2709) x AAR71380 (1-771)

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 1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 260 AACTATCAGAAATGGGAGAACAAATGTGCCAAGCTGAAATATCTCTACAAAGAAATGTG 319
 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLeuLeuSerTyrLysGluMetLeu 40
 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCCAAGCTCCAGTTATCATACCTTC 379
 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 380 CTTTGGATCAGGAACGGAGTGGTGTATGTTGGAGCAAGATCAATATTTTCATTC 439
 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisilePheSerPhe 80
 440 GACCTGTTAATATCAGATTTTCAAAGATTGTGGCCAGTATCTTACACCGAGAGA 499
 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 500 GATGAATCAAGTGGCTGGAAAGACATCCTGAAAGAAATGTGCTAAATTTTCATCAAGGTA 559
 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheileLysVal 120
 560 CTTAAGGCATATAATCAGACTCATTTGTAGCTGTGGAAACGGGGCTTTTCATCAAT 619
 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 620 TGCACCTACATTGAATTCGACATCATCTCGAGCAATATTTTAAAGCTGGAGAACTCA 679
 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 680 CATTTTGAACACGGCTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 740 TTAATAGATGGAATATATCTCTGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
 181 LeuileAspGlyLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 800 ATCTTCGAACTCTGGGACACACCAATCAGACAGAGCAGCATGATTCACGGTGG 859
 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220

860 CTCAATGATCAAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTGAACAATCTCTGAAGAT 919
 221 LeuAsnAspProLysPheIleSerAlaHisLeuileSerGluSerAspAsnProGluAsp 240
 920 GACAAAGATATCTTTTCTCCGTGAAATCCATAGATGAGAGACATCTCTGGAAGACT 979
 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 980 ACTACCGCTAGAAAGTGCAGATATGCAAGAAATGACTTTTGGAGGCGACAGAAAGTCTGTG 1039
 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
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 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuileCysSerValProGlyProAsnGly 300
 1100 ATTGACATCTAATTTTGTGAAGCTGAGATGTATCTTAATGAACCTTTAAAGATCCTAAA 1159
 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 1160 AATCCAGTTGTATATGGAGTGTTCACGACTTCCAGTAACTTTTCAAGGGATCAGCCGTG 1219
 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 1220 TGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTGTCATATGCCACAGGAT 1279
 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 1280 GGACCAACTATCAATGGTGCCTTATCAAGAGAGAGTCCCTATCCACGGCCAGGAACT 1339
 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
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 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 1400 ACCTTTGCAAGAAGTCAATCCAGCCATGATGATGTTTTCGAAACAGATGTTGGACCGCTTCTAAA 1459
 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 1460 ATAGTGATCAAAACGGATGTAATTTCAATTTACAAATTTACAAATTTGCTAGACCGAGTGGAT 1519
 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 1520 GCAGAGATGACACAGTATGATGTTTATCGGAACAGATGTTGGACCGCTTCTTAAA 1579
 441 AlaGluAspGlyGlnTyrAspValMetPheileGlyThrAspValGlyThrValLeuLys 460
 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGGAAGAAATG 1639
 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
 1640 ACAGTTTTCGGGACCGACTGCTATTTTCAGCAATGGAGCTTTCACCTAAGCAGCAACAA 1699
 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrIleGlnGln 500
 1700 CTATATATTTGTTTCAACGGCTGGGTTTCCAGCTCCCTTTTACACCGGTGTGATTTTAC 1759
 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 1760 GGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTCTGCTGGATGGTCT 1819
 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 1820 GCATGCTCTCGCTATTTTCCCACTCAAGAGAGCCACAAAGACCAAGATATTAAGAAAT 1879
 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
 1880 GGAGACCCACTGACTCTGCTGTTTACAGTTCACCATGATTAATCAATGCGCACGCCCT 1939
 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
 1940 GAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGAAATGCAGTCCGAG 1999

Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
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 Db 241 AspLysValTyrPhePhePheGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGTAATAGGTGAGATATGCAAGATGACTTTGGAGGCGCAGAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisSerLeuVal 280
 QY 1040 AATAATGGACAACATCTCTAAAGCTGCTGATTTGCTCAGTCGCCAGGTCCTCAATGGC 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTGTCAGCACTGAGGATGATTCCTTAATGAACTTTAAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelLysAspProLys 320
 QY 1160 AATCCAGTTGTATATGGAGTGTATACGACTTCCAGTTACATTTTCAAGGGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePhelLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGATGAGAGGGTGTCTTCCTGTCATATGCCACAGGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCACTATCAATGGTGGCTTATCAAGAGAGTCCCTATCCAGCGCCAGAACT 1339
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 QY 1340 TGTCCAGCAACATTTGGTGGTGTGACTTCAAAAGGACCTTCCCTGATGATGTATA 1399
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 QY 1580 GTAGTTTCAATTCCTAAGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGNACCGACTCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
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 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAAGCTGTCTGAGTGTTCCTTCGCCGAGACCTTACTGTCTGGATGTTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
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 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATAATCACCATGCGCCACAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGAAATCATCTATGCTGATGAGAAATAGTAGCACAATTTTGAATGCGAGTCCGAAG 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600

QY 2000 TCGCAGAGCGCTGGTCTATTGGCAATTCAGAGCGGAAATGAAGACGCAAGAAAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTACGTAGTCTCAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGGATTCAGCAATTTACCTCTGCCATCGGTGGAAACATGGTTCATACAAACTCTT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGGTAAACCTCGGAAGTCAATTCACACAGAGCATTTTGGAGAACTTCTTCATAAAGAT 2239
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGAGATGGCTCTTAAGACCAAAATATGCTCAATAGCATGACACCTAGCCAGAAG 2299
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCTGTACAGACTTTCATCAGCTCATCAACACCCCAATCTCAACACGATGGATGAG 2359
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAGTTTGGAAAAAGGACCCGAAAAACAACCTCGGCAAGGCCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGAAACAGTAAACAAATGGAAGCACTTCAAGAAATAAGAAAGGTAGAAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGlnAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAAATTTGAGAGGCGCACCCAGGAGTCTC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 3
 ID ABG96413 standard; protein; 771 AA.
 AC ABG96413;
 DT 11-DEC-2002 (first entry)
 DE Human ovarian cancer marker M473.
 KW Human; ovarian cancer; marker; cancer; familial history; brain disorder;
 KW central nervous system disorder; bacterial meningitis; viral meningitis;
 KW Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
 KW brain herniation; inflammation; encephalitis; testicular disorder;
 KW nontuberculous granulomatous orchitis; connective tissue disorder;
 KW heart disorder; ischaemic heart disease; atherosclerosis; neoplasm;
 KW histological type; carcinogenic; ovarian cancer marker.
 OS Homo sapiens.
 PN WO200271928-A2.
 PD 19-SEP-2002.
 XX 14-MAR-2002; 2002WO-US007826.
 XX 14-MAR-2001; 2001US-0276025P.
 PR 14-MAR-2001; 2001US-0276026P.
 PR 10-AUG-2001; 2001US-0311732P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 26-SEP-2001; 2001US-0324967P.
 PR 26-SEP-2001; 2001US-0325102P.
 PR 26-SEP-2001; 2001US-0325149P.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX

PI Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG;
PI Meyers RE, Morrissey MP, Olandt PU, Sen A, Vieby PO, Mills GB;
PI Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
XX DR N-PSDB; ABS76512.
XX WPI: 2002-723277/78.
XX DR N-PSDB; ABS76512.
XX Assessing whether a patient is afflicted with ovarian cancer, useful in
PT assessing the stage or progression of the disease, comprises comparing
PT the expression level of a cancer marker in a sample from a patient and
PT from a non cancer patient.
XX Disclosure; Page 401-402; 481pp; English.
XX The present invention relates to a new method for assessing whether a
CC patient is afflicted with ovarian cancer. The method involves comparing
CC the expression level of a marker in a patient sample and the normal level
CC of expression of the marker in a control non-ovarian cancer sample, where
CC the marker is selected from 363 cancer markers described in the
CC specification. The method of the invention is useful in diagnosing or
CC characterizing cancer, in detecting the presence of cancer as early as
CC possible, and the recurrence of ovarian cancer. The method may also be of
CC particular use with patients having an enhanced risk of developing
CC ovarian cancer (e.g. patients having a familial history of ovarian
CC cancer). The cancer markers may be used in the management and treatment
CC of e.g. brain and central nervous system disorders (e.g. bacterial and
CC viral meningitis, Alzheimer's disease or Parkinson's disease), brain
CC disorders (e.g. cerebral oedema, hydrocephalus or brain herniations),
CC inflammations (e.g. bacterial or viral meningitis or encephalitis),
CC testicular disorders (e.g. non-tuberculous granulomatous orchitis),
CC connective tissue disorders, or heart disorders (e.g. ischaemic heart
CC disease or atherosclerosis). The compositions and methods may also be
CC used in assessing the histological type of neoplasm associated with
CC ovarian cancer, monitoring the progression of ovarian cancer, determining
CC whether ovarian cancer has metastasized or is likely to metastasize,
CC selecting a composition for inhibiting ovarian cancer, assessing the
CC ovarian carcinogenic potential of a compound, or inhibiting ovarian
CC cancer or at risk of developing ovarian cancer. The present amino acid
CC sequence represents one of the ovarian cancer markers described in the
XX invention
XX Sequence 771 AA;
Alignment Scores:
Score: 0 Length: 771
Pred. No.: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 5 Gaps: 0
US-09-774-490-1 (1-2709) x ABG96413 (1-771)
QY 200 ATGGGCTGGTAACTAGGATGCTGCTCTTTCTGGGGAGTATTACTTACAGCAGAGCA 259
Db 1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAGAACAAATGCGCAAGCTGAAATATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValileThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACCGAGTAGGCTGTATGTTGGAGCAAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisilePheSerPhe 80
QY 440 GACCTGTTAATATCAAGATTTTCAAAGATTTGTCGCCAGTATCTTACACCGAAGA 499
Db 81 AspLeuValAsnileLysAspPheGlnLysileValTrpProValSerTyrThrArgArg 100

QY 500 GATGAATGCAAGTGGCTGGAAAAACACATCTCTGAAAGAAATGTGCTAATTTTCATCAGGTA 559
Db 101 AspGluCysLysLysTrpAlaGlyLysAspileLeuLysGluCysAlaAsnPheileLysVal 120
QY 560 CTTAAGGCGATATAATCAGACTCAGCTTGTACGGCTGTGGAACGGGGCTTTTTCATCAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGACTCA 679
Db 141 CysThrTyrIleGluileGlyHisProGluAspAsnilePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACGGCGCTGGAGAGTCCATATGACCCCTAAGCTGCTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATTTACTCTCGAAGCTGAGCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuileAspGlyLysLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTTGGGCACACCCCAATCAGGACAGACAGATGATTCAGGCTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTtp 220
QY 860 CTCATGATCCAAAGTTTCAATAGTCCACCTCATCTCAGAGAGTGCACATCTCTGAGAT 919
Db 221 LeuAsnAspProLysPheileSerAlaHisLeuileSerGluSerAspAsnProGluAsp 240
QY 920 GACAAGTATATCTTTCTTCGTCGAAATGCAATAGATGAGAGACACTCTCGAAAGCT 979
Db 241 AspyLysValTyrPhePhePheArgGluAsnAlaileAspGlyGluHisserGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGTGCAGATATGCAAGAAATGACTTTTGGAGGGCAGCAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnileCysLysAsnAspPheGlyGlyHisargSerLeuVal 280
QY 1040 AATAATGGAACAATCTCTCAAAGCTGCTGTGATTTGCTAGTCCAGGTCAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuileCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGAACTGCGAGGATGTTCTCTTAATCAACTTTTAAAGATCTCTAAA 1159
Db 301 IleAspThrHisAspAspGluLeuGlnAspValPheLeuMetAsnPhelysAspProLys 320
QY 1160 AATCAGCTGTATATGAGAGTGTTTACGACTTCCAGTAAATTTTCAAGGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnilePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTCATATGGTGGCTTTTCAAGGAAGAGTCCCTTATCCAGCCGAGCAACT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCAGCAAAACAACTTTGGTGGTGTTCCTCTACAAAGAGCTTCTCTGATGATGTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValile 400
QY 1400 ACCTTTGCAAGAGTATCCAGCCATGTACATCCAGTGTTCCTTATGAAACATCCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTTACAAATTTGCTAGACCCGAGTGGAT 1519
Db 421 IleValileLysThrAspValAsnTyrGlnPheThrGlnileValValAspArgValAsp 440
QY 1520 GCAGAGAGTGGACAGTATGATGTTATGTTTATCGGAACAGAGTGTGGGACCGTCTCTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheileGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAGAGGTTCTCTGGAAGAAATG 1639

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Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTCCACATAAGCAGCAAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATTGGTTCAACGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGTCTGAGTGTTCCTCCGCGAGACCCCTTACTGCTGGTGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGTATTTTCCCACTCAAGAGACGACAGACGACAGCAAGATAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTCAGCTGTTTCCAGCTTACACCATGATATACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGATGCGATCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGCCGCTGCTTATTTGGCAATTCAGAGCGCAATAGAGCGCAAAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluGluGluGlu 620
Qy 2060 ATCAGAGTGATGATCATATCATATCAGGACAGATCAAGGCTTCTGCTAGTGTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlnLeuLeuArgSerLeuGln 640
Qy 2120 CAGAAGGATTCAGGCAATTAATCTCTGCCATGCGGTGGAAACATGGTTTACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAGGTAAACCTGGAGTCAATTCACAGAGCATTTTGGAGAACTTCTTCATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
Qy 2240 GATGATGAGATGGCTTAAAGACCAAGAAATGTCCAATAGCATGACACTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGTTACAGAGCTTCATGAGCTCATCAACCCACCCCAATCTCAACACGATGGATGAG 2359
Db 701 ValTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGAACAAGTTTGGAAAGGNCAGAAACACACGTCGCGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATAAGAAAGCTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
Qy 2480 ACCCAGCAATTTGAGAGGCGACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
```

RESULT 4
ADD08934

ID ADD08934 standard; protein; 771 AA.

XX AC

XX ADD08934;

XX 01-JAN-2004 (first entry)

XX Human semaphorin 3A protein. SEQ ID NO:10.

XX

KW screening; modulator; binding; neuropilin growth factor receptor;
KW vascular endothelial growth factor C;
KW vascular endothelial growth factor 3; VEGF-C; VEGFR-3;
KW neuropilin; cytostatic; neurotropic; neuroprotective; vulnerary;
KW vasotropic; cardiac; angiogenic process; nervous system growth;
KW nervous system function; cancer; ischaemia; cerebral infarction;
KW cerebral bleeding; Alzheimer's disease; myocardial infarction; human.
XX Homo sapiens.
XX WO2003029814-A2.
XX 10-APR-2003.
XX 01-OCT-2002; 2002WO-EP011069.
XX 01-OCT-2001; 2001US-0326326P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX Alitalo K, Karkkainen M, Karila K;
XX WPI; 2003-381660/36.
XX N-PSDB; ADD08933.
XX Screening for modulators of neuropilin and vascular endothelial growth
XX factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction
XX of neuropilin and VEGFR-3 or VEGFR-3 in the presence and absence of a
XX modulator compound.
XX Disclosure; SEQ ID NO 10; 181pp; English.

The present invention describes a method of screening for modulators of
binding between a neuropilin growth factor receptor and a vascular
endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising
comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the
presence and in the absence of a putative modulator compound. Also
described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-
3 or neuropilin biological activity; (2) modulating growth, migration or
proliferation of cells in a mammalian organism; (3) a bispecific antibody
which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3
polypeptide; (4) modulating neuronal growth or neuronal scarring in a VEGF
mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF
-C that binds to a neuropilin receptor. The modulators have cytostatic,
neurotropic, neuroprotective, vulnerary, vasotropic and cardiac
activities. The method is useful in modulating angiogenic processes and
nervous system growth and function, such as in the treatment of cancer,
wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or
myocardial infarction. The polypeptide comprising a fragment of a VEGF-C
that binds to a neuropilin receptor, is useful for manufacturing a
medicament for the treatment of diseases characterised by aberrant
growth, migration or proliferation of cells that express a neuropilin
receptor. The present sequence represents human semaphorin 3A, which is
used in the exemplification of the present invention.

Sequence 771 AA;

Alignment Scores:

Pred. No.:	0	Length:	771
Score:	4201.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	7	Gaps:	0

US-09-774-490-1 (1-2709) x ADD08934 (1-771)

Qy 200 ATGGGCTGGTTAACTAGGATTTCTGCTTTTCTGGGAGTATTACTTACAGCAAGCA 259

Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

Qy 260 AACTATCAGATGGGAAGAACAAATGTGCCAGGCTGAATTTATCTTACAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAAACGGATAGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAAATCAAGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValIleProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCCTGAAAGAATGTCTTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCACTGTAGCGCTGTGGAAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTCAATTCGACATCATCTCGAGGCAATATTTTAAAGCTGGAGACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACACGGCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAATATATCTCTGAACTGACGCTGATTTTATGGGGCAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ACTTCCGAACTTTGGGCACACCAACCAATCAGGACAGACAGCATGATTTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCAATAGTGCACCTCATCTCAGAGAGTGACATCTCGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACCTTTTTCCTCGTGAATGCAATAGATGGAACACACTCTGGAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGGTGAGATATGCAAGAATGACTTTGGAGGGCAGAACTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAATGACACATTCCTCAAAGCTCGCTGATTTGCTCAGTGCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTATGAATCGAGGATGTATCTTAATCAACTTTAAAGATCTTAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGGAGTTTACGACTTCAGTAAACATTTTCAAGGATCAGCCGG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGTGAGAAGGTGTTCTTGGTCCATATGCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGGCAGGAAC 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCAGCAAAACATTTGGTGGTTTGTACTCTCAAAAGGACCTTCTCTGATGTTATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTGTTCTTATGAAACATGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGATGTAATATCAATTTTACAAAATTTGCTGAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGACACGATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTCTGCTGGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTTCCGGAACCGACTGCTATTTTTCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrThrLysGlnGln 500
QY 1700 CTATATATTGGTTCAACGGCTGGGTGCTCCAGCTCCCTTTTACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTTTGGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACGACGACGACGACGACGACGACGAC 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTGCTGTTTACAGCTTACACCATGATTAATCACCATGCGCACGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAATCATCTATGGTGTAGAGAAATAGTAGACATTTTGGAAATGCAAGTCCG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGCTGGTCTTATTTGGCAATTCGAGCGGCAATGAAAGCGCAAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGCTGAGTATCATATCATCAGCAGATCAAGCGCTTCTGCTAGTGTACTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAACATGGGTTCATACAACTCT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACCTCGAAGTCAATCAGCAGAGCAATTTGGAAGAATCTTCTTCAAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTTACAGAGACTTTCATGAGTCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTyrTyrArgAspPheMetGlnLeuLeuAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAAGTTTGGAAAAGGACCGAAACACCTGCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValIleTyrLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAAACAGTAACAATGGAGCATTCAAGAAAATAAGAAAAGTTGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCCAGCAATTTGAGAGGCGACCCAGGAGTGC 2512
 |||||
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 5
 ADE25760
 ID ADE25760 standard; protein; 771 AA.

XX ADE25760;
 AC
 XX 29-JAN-2004 (first entry)
 DT
 XX Human protein differentially expressed in foam cells #37.

XX Human; differential expression; foam cell; LPS; lipopolysaccharide;
 KW cardiovascular disease; atherosclerosis.

XX Homo sapiens.

XX US2003194721-A1.

XX 16-OCT-2003.

XX 18-SEP-2002; 2002US-00247671.

XX 19-SEP-2001; 2001US-0323784P.

XX (INCY-) INCYTE GENOMICS INC.

PA Mikita T, Shiffman D, Porter JG, Kaser MR;

PI WPI: 2003-875398/81.

DR N-PSDB; ADE25679.

XX Combination containing several polynucleotide that are differentially
 PT expressed in foam cells and complements of the polynucleotides, useful
 PT for diagnosing cardiovascular disease or atherosclerosis.

PS Disclosure; SEQ ID NO 164; 37pp; English.

XX The invention relates to a combination comprising several polynucleotides
 CC having any one of 127 sequences (S1) such as the sequence of human
 CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
 CC hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit
 CC mRNA, etc., and their complements. The cDNAs are differentially expressed
 CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
 CC obtaining an extended or full length gene from a library of nucleic acid
 CC sequences, an expression vector containing the nucleic acids, a host cell
 CC containing the vector, a purified polypeptide appearing as ADE25750 and
 CC ADE25751, producing a protein by culturing the host cell, and a
 CC composition comprising a purified antibody that specifically binds to the
 CC proteins. The foam cell-expressed nucleic acids are useful for a high
 CC throughput detection of differential expression of one or more
 CC polynucleotides in a sample. The sample is from a subject with
 CC atherosclerosis and comparison with a standard defines early, mid or late
 CC stages of the disorder. The foam cell-expressed nucleic acids are useful
 CC for high throughput screening of a library of molecules or compounds to
 CC identify a ligand which binds a polynucleotide. The library is chosen
 CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
 CC useful for a high throughput screening of library of molecules or
 CC compounds to identify at least one ligand which specifically binds a
 CC protein, for purifying a ligand from a sample for making an antibody. The
 CC foam cell-expressed nucleic acids are useful for diagnosing
 CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
 CC as elements on a microarray which can be used for detecting related
 CC polynucleotide in a sample, diagnosing cardiovascular disease,
 CC atherosclerosis. The present sequence represents a protein differentially
 CC expressed in LPS treated foam cells.

XX Sequence 771 AA;

SQ Alignment Scores:

Pred. No.:	0	Length:	771
Score:	4201.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	7	Gaps:	0
US-09-774-490-1 (1-2709) x ADE25760 (1-771)			
QY	200	ATGGGCTGGTTAACTAGGATTGCTCTTTCTCTGGGAGTATTACTTACAGCAGACGA	259
Db	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThraAlaGala	20
QY	260	AACTATCAGAATGGGAACAATGTGCAAGGCTGAAATTTATCTCAAAAGAATGTG	319
Db	21	AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAACAATGTGATCATTCAATGGCTGGCCACAGCTCCAGTTATCATCACTTC	379
Db	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGGAAACGGAGTAGCTGTATCTTGGAGCAAAAGGATCACATATTTTCATTC	439
Db	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACAGAAGA	499
Db	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGTAATTTTCAATCAAGTA	559
Db	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATATACAGACTCACCTGTGACGCTGTGGAACGGGGCTTTTCATCCAATT	619
Db	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTGAAATGGACATCATCTCGAGACACAATATTTTAACTCGAGAACTCA	679
Db	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT	739
Db	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThraAlaSerLeu	180
QY	740	TTAATAGATGAGAAATATATCTCTGGAACCTGAGCTGATTTTATGGGCGAGACTTGTCT	799
Db	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCCAACTCTTTGGCCACCCACCACCAATCAGGACAGACAGCATGATTCCAGGTGG	859
Db	201	IlePheArgThrLeuGlyHisHisIleProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAACTCTCAAGAT	919
Db	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATATCTTTCTTCGTAAGTAAATGCAATAGATGGAGAACACTCTCGAAAAGCT	979
Db	241	AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGATAGGTACAGATATGCAAGAAATGACTTTGGAGGCGCACAGAGTCTGGTG	1039
Db	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280
QY	1040	AATAAATGGACAACTTCTCAAGCTGCTGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTG	1099
Db	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTGTGAACTGAGGATGTATTCTTAATGAATCTTAAAGATCCTAAA	1159
Db	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320

QY 1160 AATCCAGTTGATATGAGTGTTCAGACTTCAGTAACATTTTCAGCGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLeuGlySerAlaVal 340
 QY 1220 TGTATATAGCATGATGATGAGAGGGTGTCTCTTGGTCCATATATCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCAACTATCAATGGTGTCTTATCAAGAGAGTCCCTTATCCAGCCGAGAACT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTGGTGTGTGTCTCTCAAGAGACCTCTCTGATGATTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY 1400 ACCTTTGCAAGAAGTCCATCCAGCATGTACAATCCAGTGTCTTCCATGAACAATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACCGGATGTAATTATCAATTTACAAATTTGTCGTAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAAGATGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGAGACTGCTGATGATGATGATGATGATGATGATGATGAT 1639
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGGAACCGACTGCTATTTCCAGCAATGGAGCTTTCCACTAAGCAGCAACAA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTTGGTTCAACCGCTGGGTGCTCCAGCTCCCTTTTACACGGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAGCTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
 Db 521 GlyLysAlaCysAlaGluCysLysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGACAGACGACAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGGATCATATCATATCATATCATATCATATCATATCATATCATATCATAT 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGGATTCAGGCATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGGTAACTGGAAGTCTTGAACAGAGCATTTTGAAGAAGTCTTCTTCAATAAGAT 2239
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCAGAAG 2299

Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCTGCTACAGAGACTTTCATGCTCAGCTCATCAACACCCCAATCTCAACACGATGGATGAG 2359
 Db 701 ValTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGTAACAATTTGGAAAAAGGACCGAAAAACAACGTCGCGCAAGCCAGGACATACC 2419
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGGACAGTAACAATTTGGAGACCTTACAGAAATTAACAAGGTTAGAACACGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
 QY 2480 ACCACCAATTTGAGAGGCGACCCAGGAGTGTCT 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 6
 ID ADQ19751
 XX ADQ19751 standard; protein; 771 AA.
 AC ADQ19751;
 XX 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2570.
 XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 OS Homo sapiens.
 XX WO2004048938-A2.
 XX 10-JUN-2004.
 XX 26-NOV-2003; 2003WO-US038193.
 XX 26-NOV-2002; 2002US-0429739P.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX A&iz N, Ginsburg WM, Zlotnik A;
 XX WPI; 2004-441208/41.
 XX Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.
 XX Example 2; SEQ ID NO 2570; 210pp; English.
 XX The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
 SQ Sequence 771 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches:

Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	8	Gaps:	0
US-09-774-490-1 (1-2709) x ADQ19751 (1-1771)			
QY	200	ATGGCTGGTTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGCAAGACA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACTATCAGATGGGAAGAACAAATGTGCCAAGCTGAAATATCTCTACAAAGAATGTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAATGTGATCACTTCTCAATGGCTGGCCACAGCTCCAGTTATCATACCTTC	379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGCAACGGATAGGCTGTATGTGGAGCAAGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGGTTAATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGATGTCTAAATTTTCATCAAGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCATCCAAT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTTGAAATGGACATCATCTCTGAGGCAATATTTTAAAGCTGGAGA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CAATTTGAAACGGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGGAATATTACTCTGGAATCGAGCTGATTTTATGGGGAGACTTTGCT	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCGAATCTTGGGCACCAACCAATCAGGACAGACAGATGATTCAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGATGACAAATCCTGAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATCTTTTCTTCCTCGTGAATGCAATAGATGGAGAACACTCTCGAAAAGCT	979
DB	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTPAGATAGGTGAGATATGCAAGAATGACTTTGGAGGGCAGAAAGTCTGGTG	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal	280
QY	1040	ATAAATGACACATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCCAATGGC	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTTCATCACTGAGGATGTATTCCTAATGAACCTTTAAAGATCCTAAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	ATCCAGTTGTATATGGAGTGTATACGACTTCAGTTAAACATTTTCAAGGGATCAGCCGTG	1219

DB	321	AsnProValValTyrGlyValPheThrThrSerSerSerSerSerSerSerSerSerSer	340
QY	1220	TGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGA	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCCCGCAAAACATTTGGTGGTTTGACTCTCAAGAGACCTTCTCTGATGATGTTATA	1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle	400
QY	1400	ACCTTTTGCAGAAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAAATCG	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGATCAAAACGGATGTAATTTTCAATTTTACAAATTTGCTGTAAGCCGAGTGGAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGACAGTATGATGTTATCGAAACAGATGTTGGACCGTCTCTTAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	CTAGTTTCAATTCCTAAGGAGACTTGTATGATTTTAGAAGAGGTTCTCTCGAAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCACCTAAGCAGCA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln	500
QY	1700	CTATATATTTGCTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTGATTTTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGluLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAAGCGTGTGCTGAGTGTGGCTCGCCCGAGACCTTACTGTGTGGAGTGTCT	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCATGTTCTCGTATTTTCCACTGCAAGAGACGACACAGCAGACAGATATAAGAAAT	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn	560
QY	1880	GGAGACCCACTGACTCTGCTTCCAGCTTACACCATGATAATCACCTGGCCACAGCCT	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro	580
QY	1940	GAAGAGAAATCATCTATGTTGAGAGAAATAGTACACATTTTGGAAATGCGTCCGAAG	1999
DB	581	GluGluAlaGlyIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys	600
QY	2000	TCGCAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGCAATTAAGAGCGGAAAGAGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATGATCATATCAGGACAGATCAAGGCTTCTGCTAGTAGTGTACAA	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640
QY	2120	CAGAAGGATTCAGGCAATTTACTCTCTGCCATCGGTGGAAACATGGGTTCATACAACTCT	2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu	660
QY	2180	CTTAAGGTAAACCTCGGAAGTCAATGACACAGAGCAATTTGGAAGAACTTCTTCATAA	2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp	680
QY	2240	GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTACCCAGAG	2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys	700

QY 2300 GTCTGTACAGAGCTTCATGAGCTCATCAACCCCACTCTCAACAGATGATGAG 2359
 |||||
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 |||||
 QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGAACAACACGTCGCGAAGGCCAGGACATACC 2419
 |||||
 Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 |||||
 QY 2420 CCAGGGAACAGTAACAAATGGAAGACATTCACAGAAATAAGAAAGCTAGAAACAGGAGG 2479
 |||||
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
 |||||
 QY 2480 ACCACGAATTTGAGAGGACCCAGGAGTGTC 2512
 |||||
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 |||||
 RESULT 7
 ADN95333
 ID ADN95333 standard; protein; 770 AA.
 AC ADN95333;
 XX
 XX 01-JUL-2004 (first entry)
 XX
 DE Human BEC/LEC-related protein sequence SeqID255.
 XX
 KW growth; differentiation; blood endothelial cell; BEC;
 KW lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
 KW lymphatic growth agent; VEGF-C; VEGF-D; angiogenic; cytostatic;
 KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003080640-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 07-MAR-2003; 2003WO-US006900.
 XX
 PR 07-MAR-2002; 2002US-0363019P.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
 XX
 DR WPI; 2003-876899/81.
 DR N-PSDB; ADN95334.
 XX
 PS Example 1; SEQ ID NO 255; 176pp; English.
 XX
 CC This invention relates to a method of differentially modulating the
 CC growth or differentiation of blood endothelial cells (BEC) or lymphatic
 CC endothelial cells (LEC) comprises contacting endothelial cells with a
 CC composition comprising an agent that differentially modulates blood or
 CC lymphatic endothelial cells. Treating hereditary lymphoedema comprises
 CC identifying a human subject with lymphoedema and with a mutation in at
 CC least one allele of a gene encoding a LEC protein, where the mutation
 CC correlates with lymphoedema in human subjects, and with the proviso that
 CC the LEC protein is not VEGFR-3; and administering to the subject a
 CC composition comprising a lymphatic growth agent selected from VEGF-C or
 CC VEGF-D polypeptides and polynucleotides. The invention may be useful for
 CC the development of compounds with an angiogenic, cytostatic,
 CC vasotropic or antiinflammatory activity or for gene therapy. The method
 CC is useful in modulating the growth or differentiation of blood
 CC endothelial cells or lymphatic endothelial cells, in treating hereditary
 CC lymphoedema, in screening for an endothelial cell disorder or
 CC predisposition to the disorder or in monitoring the efficacy or toxicity
 CC of a drug on endothelial cells. The agent is useful in manufacturing a
 CC medicament for the differential modulation of blood vessel endothelial
 CC cell or lymphatic vessel endothelial cell growth or differentiation. The

CC lymphatic growth agent may also be used in manufacturing a medicament for
 CC the treatment of hereditary lymphoedema resulting from a mutation in a
 CC LEC gene or of other diseases involving the lymphatic vessels, such as
 CC various inflammatory diseases and cancer metastasis via the lymphatic
 CC system. The present sequence is that of a human LEC/BEC differentially
 CC expressed protein which is related to the method of the invention. Note:
 CC this sequence does not appear in the specification but was obtained by
 CC the indexer using the source data given in table 14 of the specification.
 XX
 SQ Sequence 770 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 770
 Score: 4197.00 Matches: 770
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.72% Indels: 0
 DB: 7 Gaps: 0

US-09-774-490-1 (1-2709) x ADN95333 (1-770)

QY 200 ATGGGCTGGTTAACTAGGATTGCTGTCTTTCTGGGAGTATTACTTACAGCAAGCA 359
 |||||
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaGAla 20
 |||||
 QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319
 |||||
 Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 |||||
 QY 320 GAATCCAAATGTGATCATCTTCAATGGCTTGGCCACAGCTCCAGTATCATACCTTC 379
 |||||
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 |||||
 QY 380 CTTTGGATGAGCAACGAGTAGGTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
 |||||
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAsnHisIlePheSerPhe 80
 |||||
 QY 440 GACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGTGCCAGTATCTTTACACCAAGA 499
 |||||
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 |||||
 QY 500 GATGAATGCAGTGGGCTGGAAACACATCTCTGAAGATGCTGTAATTTTCATCAAGTA 559
 |||||
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 |||||
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTGACGCTGTGGAACGGGCTTTTCATCAAT 619
 |||||
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 |||||
 QY 620 TGCACCTACATTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
 |||||
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 |||||
 QY 680 CATTTTGAACACGGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739
 |||||
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 |||||
 QY 740 TTAATAGATGGAAGATTTACTCTGAACTGCAGCTGATTTTATGGGGGAGACTTTGCT 799
 |||||
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 |||||
 QY 800 ATCTCTCCGAACCTTTTGGGCACCCACCAATCAGGACAGACAGCATGATTTCCAGGTGG 859
 |||||
 Db 201 IlePheArgThrLeuGlyHisHisIleProIleArgThrGluGlnHisAspSerArgTrp 220
 |||||
 QY 860 CTCATATGATCAAAAGTTTATAGTCCACCTCATCTCAGAGAGTGCACATCTCTAGAT 919
 |||||
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 |||||
 QY 920 GACAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979
 |||||
 Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 |||||

QY 980 ACTCAGCTAGATAGGTGACATATGCAAGATGACTTTGGAGGCGCACAGAGTCTGGTG 1039
 DB 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGACAACTATCTCTAAAGTCTGCTGATTTGCTAGTCCAGGTCCTCAATGGC 1099
 DB 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTGATCACTGAGGAGTGTATTCCTTAATGAATTTAAAGATCCTAAA 1159
 DB 301 IleAspThrHisPheAspGlnLeuGlnAspValPheLeuMetAsnPhelLysAspProLys 320
 QY 1160 AATCAGCTTGATATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAG 1219
 DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAG 1279
 DB 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCAACTATCAATGGTGGCTTATCAAGAGAGTCCCTATCCAGGCGCAGGAAT 1339
 DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGAGCTTCTCTGATGATGTATA 1399
 DB 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAAGATCATCCAGCATGTAATTCAGTGTTCCTTATGAAACATCGCCCA 1459
 DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTATCAAAACCGATTAATATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
 DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 CGAAGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGTGTCTGCTGGAAGATG 1639
 DB 461 ValValSerIleProLysGlnThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGGACCGACTCTATTTACAGCAATGGAGCTTCCACTAAGCAGACAA 1699
 DB 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
 DB 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAAGCTGTGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
 DB 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTCTCGCTATTTTCCACTGCAAGAGACGACAGACGACAGATATAAGAAAT 1879
 DB 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTGCTTACACTTTACACCATGATTAATCACCATGGCCACAGCCCT 1939
 DB 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATATGCTGTAGAGATAGTAGACATTTTGGATGCGAGTCCGGAAG 1999
 DB 581 GluGluArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 600
 QY 2000 TCGCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
 DB 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGATGGATGATCATATCATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119

DB 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGATTTCAGCAATTACTCTGCCATCGGTGGACATGGGTTTCATACAACTCTT 2179
 DB 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGGTAAACCTGGAGTCAATGACACAGACATTTGGAAGAACTTCTTCATAAAGAT 2239
 DB 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGAGATGCTCTTAAGACCAAAAGAAATGTCATAGCATGACACCTAGCCAGAAG 2299
 DB 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCTGGTACAGACTTCATGCTCAGTCTCAACACCCCAATCTCAACACCATGATGAG 2359
 DB 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAAGTTTGGAAAAGGACCGAAACAAACGTCGCGCAAGCCAGGACATACC 2419
 DB 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGAAACAGTAAACAAATGGAAGCATTCAAGAAATAAGAAAGGTAGAAACAGGAGG 2479
 DB 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAAATTTGAGAGGCGACCCAGGAGT 2509
 DB 761 ThrHisGluPheGluArgAlaProArgSer 770
 RESULT 8
 ID AAY21264
 AC AAY21264; standard; protein; 796 AA.
 XX AAY21264;
 DT 22-JUL-1999 (first entry)
 XX Human semaphorin III wild type protein fragment 1.
 DE Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin 1; presenilin 2; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX Homo sapiens.
 OS WO9845322-A2.
 XX 15-OCT-1998.
 XX 02-APR-1998; 98WO-IB000705.
 XX 10-APR-1997; 97US-0043163P.
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX (UYOT-) RIJKSONIV UTRECHT.
 XX Van Leeuwen FW, Grosveld FG, Burbach JPH;
 XX WPI; 1998-609901/51.
 XX N-PSDB; AAX75767.
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 corresponding protein mutations - used to diagnose cancer and

neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.

Disclosure; Fig 16; 258pp; English.

This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins tau and Big tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-B, neurofilament-M, neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGp-C) and neuroendocrine specific protein A

Sequence 796 AA;

Alignment Scores:

Pred. No.:	0	Length:	796
Alignment Scores:		Matches:	773
Score:	4194.00	Conservative:	0
Percent Similarity:	97.48%	Mismatches:	0
Best Local Similarity:	97.48%	Indels:	20
Query Match:	85.66%	Gaps:	1
DB:	2		

US-09-774-490-1 (1-2709) x AAY21264 (1-796)

194	QY	TGCAGCATGGGCTGGTTAACTAGGATGCTGTCTTTTCTCGGGAGTATTACTTACAGCA	253
4	Db	CysSerMetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAla	23
254	QY	AGACCAACTATCAGAATGGGAAGNACAAATGTGCCAAGGCTGAAATTTCTTACAAAGNA	313
24	Db	ArgAlaAsnTyrlGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGlu	43
314	QY	ATGTGTGAATCCAAACAATGTGATCACTTTCATGTGCTTGGCCAAACAGCTCCAGTTTATCAT	373
44	Db	MetLeuGluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHis	63
374	QY	ACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTT	433
64	Db	ThrPheLeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePhe	83
434	QY	TCATTGACCTGGTTAATATATCAAGGATTTTCAAAGATTGTGTGCCAGTAGTATCTTACACC	493
84	Db	SerPheAspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThr	103
494	QY	AGAAGAGATGAATGCAAGTGGCTCGAAAGACATCCTGAAAGATGTGCTAAATTTTCATC	553
104	Db	ArgArgaspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIle	123
554	QY	AAGGTACTTAAGGCATATAATCAGACTCACTTGTATCGCTGTGGAAACGGGGCTTTTCAT	613
124	Db	LysValLeuLysAlaTyraAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHis	143
614	QY	CCAAATTTGCACCTACATTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAG	673
144	Db	ProIleCysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGlu	163
674	QY	AACTCACATTTTGAACCGCGCTGGGAAGAGTCCCATATGACCTTAAGCTGTGCAGCA	733
164	Db	AsnSerHisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAla	183
734	QY	TCCCTTTTAAATAGATGGAGAATTATACCTCTGAACTGCAGAGCTGATTTTATGGGGCAGAC	793

Db 544 IleTyrGlyLeuAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAsp 563
 QY 1814 GTTCTGCAATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGAGACGACAGATATA 1873
 Db 564 GlySerAlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIle 583
 QY 1874 AGAAATGGAGACCCACTGACTCCTGCTTACAGACTTACACCATGATAATCACCAGCCAC 1933
 Db 584 ArgAsnGlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHis 603
 QY 1934 ACCCTTGAAGAGAGATCATCTATGTTAGAGATAGTAGACACATTTTGGAAATGCAAT 1993
 Db 604 SerProGluGluArgIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSer 623
 QY 1994 CCGAAGTCCAGAGACGCTGCTTATGCGCAATTCAGAGCGGAAATGAAGAGCGAAA 2053
 Db 624 ProLysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLys 643
 QY 2054 GAAGAGATCAGATGATCATATCATCATCAGACAGATCAAGGCTTCTGCTACGTAGT 2113
 Db 644 GluGluIleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuArgSer 663
 QY 2114 CTACACAGAGAGATTCAGGCAATTCCTCTCCATGCGGTGGAACATGGGTTTATACAA 2173
 Db 664 LeuGlnGlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGln 683
 QY 2174 ACTCTTCTTAAGGTAACTGCAAGTCTGATGACAGAGCATTTGGAAGACTTCTTCAT 2233
 Db 684 ThrLeuLeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHis 703
 QY 2234 AAAGATGATGATGAGATGGCTTCTAAGACCAAGAAATGTCCAATAGCATGACCTAGC 2293
 Db 704 LysAspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSer 723
 QY 2294 CAGAGGTCTGTACAGAGATTCATGAGCTCATCAACCAACCCCAATCTCAACAGATG 2353
 Db 724 GlnLysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMet 743
 QY 2354 GATGAGTCTGTGAACAAGTTTGGAAAGGGACCGAAACACACGTCGGCAAGGCGAGGA 2413
 Db 744 AspGluPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGly 763
 QY 2414 CATACCCAGGAGCAAGTAAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAAC 2473
 Db 764 HisThrProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsn 783
 QY 2474 AGGAGACCCAGCAATTTGAGAGGGGACCCAGGAGTGT 2512
 Db 784 ArgArgThrHisGluPheGluArgAlaProArgSerVal 796

RESULT 9

AAR74175
 ID AAR74175 standard; protein; 477 AA.
 XX AC AAR74175;
 XX DT 01-NOV-1995 (first entry)
 XX DE Human collapsin.
 XX KW Collapsin; antibody; therapy.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Binding-site 9..19 /note= "antibody binding site"
 FT Binding-site 51..65 /note= "antibody binding site"
 FT FT
 FN US5416197-A.
 XX 16-MAY-1995.

XX 15-OCT-1993; 93US-00136922.
 XX 15-OCT-1993; 93US-00136922.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Luo Y, Raper JA;
 XX WPI: 1995-193478/25.
 XX N-PSDB; AAQ92331.
 XX New antibody to human collapsin - used to inhibit the activity of
 PT collapsin, to induce neurite out-growth and to treat individuals with
 PT nerve damage.
 XX Claim 2; Col 15-18; 11pp; English.
 XX An antibody capable of specifically binding at least a portion of the
 CC collapsin protein can be used to purify human collapsin and to inhibit
 CC the activity of the protein. It can be used to induce neurite outgrowth
 CC by neuronal cells and to treat individuals suffering from nerve damage
 XX SQ Sequence 477 AA;
 Alignment Scores:
 Pred. No.: 4,896-226 Length: 477
 Score: 2562.00 Matches: 472
 Percent Similarity: 99.37% Conservative: 0
 Best Local Similarity: 99.37% Mismatches: 3
 Query Match: 52.33% Indels: 0
 DB: 2 Gaps: 0
 US-09-774-490-1 (1-2709) x AAR74175 (1-477)
 QY 899 GAGAGTGAATCTGGAAGATGACAACTATACITTTTCTCCGTGAAAAATGCAATAGAT 958
 Db 2 GluHisAspAsnProGluAspLysValTyrPhePheArgGluAsnAlaIleAsp 21
 QY 959 GGAGAACACTCTGGAAGACTACTCACCTAGAAATGAGTTCAGATATGCAAGATGACTTT 1018
 Db 22 GlyGluHisSerGlyLysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPhe 41
 QY 1019 GGAGGACAGAGTCTGCTGAATAAATGGAACAACATTCCTCAAGCTCGTCTGATTTGC 1078
 Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuIleCys 61
 QY 1079 TCAGTCCAGGTCCAAATGGCATTCGACACTCATTTTGTATGAACTCCAGAGTGTATCTTA 1138
 Db 62 SerValProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeu 81
 QY 1139 ATGAACTTTAAAGATCCTAAAAATCCAGTTGTATATGAGTGTTCACGACTTCCAGTAAC 1198
 Db 82 MetAsnPheLysAspProLysAsnProValValTyrGlyValPheThrThrSerSerAsn 101
 QY 1199 ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTT 1258
 Db 102 IlePheLysGlySerAlaValCysMetTyrSerMetSerAspValArgArgValPheLeu 121
 QY 1259 GGTCATATGCCACAGGGATGGACCCAACTATCAATGGTGCCTTATCAAGGAAGTTC 1318
 Db 122 GlyProTyrAlaHisArgAspGlyProAsnTyrGlnTrpValProTyrGlnGlyArgVal 141
 QY 1319 CCCTATCCACGCCAGGAACCTTGCCAGCAAAACATTTGGTGGTGTTCACCTCAAAAG 1378
 Db 142 ProTyrProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLys 161
 QY 1379 GACCTTCTGATGATGTTTATAACCTTTTCCAAAGACTATCCAGCCATGTACAAATCCAGTG 1438
 Db 162 AspLeuProAspAspValIleThrPheAlaArgSerHisProAlaMetTyrAsnProVal 181
 QY 1439 TTTCCTATGAACAATCGCCCAATAGTGATCAAAACGGATGTAAATATCAATTTACACAA 1498

Db 159 AspLeuGlyValTyLysGluAspIlelePheLysLeuAspThrArgAsnLeuGluSer 178
 QY 692 GCGCTGGGAGAGTCCATATGACCCCTAAGCTGTGCAGACGATCCCTTTTAAATAGATGGA 751
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 QY 752 GAATATATCTCTGGAACTCGACCTGATTTATGGGCGAGACTTGTCTATCTCCGAACT 811
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
 QY 812 CTTGGG-----CACCACCACCAATCAGACAGACGACGATGATCCAGGTGGCTC 862
 Db 219 LeuGlyProThrHisAspHisIstYrIleArgThrAspIleSerGluHisTyrTrpLeu 238
 QY 863 AATGATCCAAAGTTTCATAGTCCCACTCATCTCAGAGAGTGACAAATCTCTGAAGATGAC 922
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp 258
 QY 923 AAGATATATCTTTCTTCGTCGAAATGCAATAGATGGAGACACTCTCGGAAAGCTACT 982
 Db 259 LysIleTyrPhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
 QY 983 CAGCTAGATAGTGCAGATATGCAAGATGACTTTGGAGGGCAGACAGATCTGTGTGAT 1042
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
 QY 1043 AATGAGACAACTTCCTAAAGCTGCTGATTTGCTCAGTCCAGGTCCAAATGGCAT 1102
 Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
 QY 1103 GACACTCATTTGATGAACCTGAGGATGTATTCCTTAATGAATCTTAAAGATCCTAAAT 1162
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
 QY 1163 CAGTTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATG 1222
 Db 339 ProValValTyGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
 QY 1223 ATGTATAGATGATGATGAGAGGGTGTCTTGTGTCATATCCACAGGGATGGA 1282
 Db 359 ValTySerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
 QY 1283 CCCAATCATCAATGGGTGCTTATCAAGGAGAGTCCCTATCCAGGGCAGAGACTTGT 1342
 Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
 QY 1343 CCCAGCAAAACATTTGGTGT---TTTGACTTACAAAGGACCTTCTGATGATGTTATA 1399
 Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418
 QY 1400 ACCTTTCGAAGATGATCCAGGATGATCAATCCAGTGTTCCTATGAACATCCGCCA 1459
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
 QY 1460 ATAGTGATCAAAACGGATGATAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1519
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
 QY 1520 GCAGAGATGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1579
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 QY 1580 GTAGTTTCATTTCTTAAGGACCTGATGATGATGATGATGATGATGATGATGATGATG 1639
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluValValValValLeuGluLeu 497
 QY 1640 ACAGTTTTCGGGACCACTGCTTATTTTACAGCAATGAGCTTTTCCATTAAGCAACAA 1699
 Db 498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
 QY 1700 CTATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATTTTAC 1759
 Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537

QY 1760 GGGAAAGCGTGTCTGCTGAGTGTCTGCTGCGCCGAGACCCCTTACTGTCTTGGGATGTTCT 1819
 Db 538 GlyLysAlaCysAlaAspCysLysLeuAlaArgAspProTyrCysAlaIlePheAspGlyAsn 557
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCAACAGACGACAGATATAAGAAAT 1879
 Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577
 QY 1880 GGAGACCCACTGACTCTCTTCCAGACTTACCATGATAATCACCATGCGCCACAGCCCT 1939
 Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
 QY 1940 GAACAGAGAATCATCTATGCTGTAGAGAATAGTAGACATTTTGGAAATCAGTCCGAAG 1999
 Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 QY 2000 TCGCAGAGAGCGTGTCTTATTTGGCAATTCAGAGGCGAAATGAGAGCGAAAGAGAG 2059
 Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
 QY 2060 ATCAGAGTGTGATCATATCATCATCAGACAGATCAAGCGCTTCTGCTACGTAGTCTACAA 2119
 Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
 QY 2120 CAGAGGATTCAGGCAATTTACCTCTGCGCATGCGGTGGAACATGCGTTTCATACAACTCTT 2179
 Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 QY 2180 CTTAAGGTAAACCTCGGAAGTCATTCAGACAGACATTTGGAGAACTTCTTCATAAAGAT 2239
 Db 677 ValLysLeuThrLeuAsnValIleGluAsnGlnGluMetGluAsnThrGlnArgAlaGlu 696
 QY 2240 GATCATGAGATGCTCTTAAGACCAAAATGTCCAATAGCATGACACCTAGCCAGAGAG 2299
 Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 QY 2300 GTCTGTGTACAGAGACTTTCATGCTCATCAACACCCCAATCTTCAACACATGATGATGAG 2359
 Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 QY 2360 TTCTGTGACAAAGTTTGGAAAGGACCGCAAAACAACTCGCAAGGCCAGGACATACC 2419
 Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747
 QY 2420 CCAGGCAACAGTAACAAATGGAAGCATTACAAAGAAAATAAGAAAGGTAGAAACAGGAGG 2479
 Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
 QY 2480 ACCCAC---GAATTTGAGAGGCGCCAGGAGTGTCT 2512
 Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 11
 AAY99427
 ID AAY99427 standard; protein; 777 AA.
 XX AC AAY99427;
 XX DT 08-AUG-2000 (first entry)
 XX XX Human PRO1491 (UNQ760) amino acid sequence SEQ ID NO:310.
 DE Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
 KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
 XX OS Homo sapiens.
 XX XX WO200012708-A2.
 XX PD 09-MAR-2000.
 XX XX 01-SEP-1999; 99WO-US020111.

XX	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098749P.
PR	01-SEP-1998;	98US-0098750P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099536P.
PR	09-SEP-1998;	98US-0099596P.
PR	09-SEP-1998;	98US-0099598P.
PR	09-SEP-1998;	98US-0099602P.
PR	09-SEP-1998;	98US-0099642P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099792P.
PR	10-SEP-1998;	98US-0099808P.
PR	10-SEP-1998;	98US-0099812P.
PR	10-SEP-1998;	98US-0099815P.
PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
PR	16-SEP-1998;	98US-0100584P.
PR	16-SEP-1998;	98US-0100627P.
PR	16-SEP-1998;	98US-0100661P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100710P.
PR	17-SEP-1998;	98US-0100711P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100848P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	22-SEP-1998;	98US-0101071P.
PR	22-SEP-1998;	98US-0101279P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101474P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101476P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101479P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101741P.
PR	24-SEP-1998;	98US-0101743P.
PR	29-SEP-1998;	98US-0101915P.
PR	29-SEP-1998;	98US-0101916P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102307P.
PR	29-SEP-1998;	98US-0102330P.
PR	30-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102484P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-0103314P.
PR	07-OCT-1998;	98US-0103315P.
PR	07-OCT-1998;	98US-0103328P.
PR	07-OCT-1998;	98US-0103395P.
PR	07-OCT-1998;	98US-0103396P.
PR	08-OCT-1998;	98US-0103401P.
PR	08-OCT-1998;	98US-0103633P.
PR	08-OCT-1998;	98US-0103678P.
PR	08-OCT-1998;	98US-0103679P.
PR	14-OCT-1998;	98US-0104257P.
PR	20-OCT-1998;	98US-0104987P.
PR	20-OCT-1998;	98US-0105000P.
PR	20-OCT-1998;	98US-0105002P.
PR	21-OCT-1998;	98US-0105104P.
PR	22-OCT-1998;	98US-0105169P.
PR	22-OCT-1998;	98US-0105266P.
PR	26-OCT-1998;	98US-0105693P.
PR	26-OCT-1998;	98US-0105694P.
PR	27-OCT-1998;	98US-0105807P.
PR	27-OCT-1998;	98US-0105881P.
PR	27-OCT-1998;	98US-0105882P.
PR	27-OCT-1998;	98US-0106023P.
PR	28-OCT-1998;	98US-0106178P.
PR	28-OCT-1998;	98US-0106029P.
PR	28-OCT-1998;	98US-0106030P.
PR	28-OCT-1998;	98US-0106032P.
PR	28-OCT-1998;	98US-0106033P.
PR	29-OCT-1998;	98US-0106248P.
PR	29-OCT-1998;	98US-0106384P.
PR	29-OCT-1998;	98US-0108500P.
PR	30-OCT-1998;	98US-0108464P.
PR	03-NOV-1998;	98US-0108562P.
PR	03-NOV-1998;	98US-0106902P.
PR	03-NOV-1998;	98US-0106905P.
PR	03-NOV-1998;	98US-0106919P.
PR	03-NOV-1998;	98US-0106932P.
PR	03-NOV-1998;	98US-0106934P.
PR	10-NOV-1998;	98US-0107783P.
PR	17-NOV-1998;	98US-0108775P.
PR	17-NOV-1998;	98US-0108779P.
PR	17-NOV-1998;	98US-0108787P.
PR	17-NOV-1998;	98US-0108788P.
PR	17-NOV-1998;	98US-0108801P.
PR	17-NOV-1998;	98US-0108802P.
PR	17-NOV-1998;	98US-0108806P.
PR	17-NOV-1998;	98US-0108807P.
PR	17-NOV-1998;	98US-0108867P.
PR	17-NOV-1998;	98US-0108925P.
PR	18-NOV-1998;	98US-0108848P.
PR	18-NOV-1998;	98US-0108849P.
PR	18-NOV-1998;	98US-0108850P.
PR	18-NOV-1998;	98US-0108851P.
PR	18-NOV-1998;	98US-0108852P.
PR	18-NOV-1998;	98US-0108858P.
PR	18-NOV-1998;	98US-0108904P.
XX		(GETH) GENENTECH INC.
XX		Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WT;
PI		WPI; 2000-237871/20.
XX		N-PSDB; AAA37109.
XX		New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT		PRO polypeptides, useful for screening of potential peptide or small
PT		molecule inhibitors of the relevant receptor/ligand interactions.
XX		Claim 12; Fig 176; 773pp; English.
XX		AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC		receptor or secreted PRO polypeptides given in AAY93340 to AAY99462. The
CC		transmembrane and receptor PRO proteins can be used for screening of
CC		potential peptide or small molecule inhibitors of the relevant
CC		receptor/ligand interactions. The polypeptides and nucleotide sequences
CC		encoding then have various industrial applications, including uses as
CC		pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC		primers and hybridisation probes used in the isolation of the PRO
CC		polypeptides from the present invention


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Db      697 HisGluGluGlyGlnVallys-----AspLeuLeuAlaGluSerArg 710
QY      2300 GTCTGTGTCAGAGACTTCATGCGAGCTCATCAACCCCAATCTCAACACAGCATGGATGAG 2359
Db      711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY      2360 TTCTGTGAACAAGTTTGGAAAGGACCGAAACACAGCTCGCGAAAGGCCAGGACATACC 2419
Db      730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY      2420 CCAGGGAACAGTAACAATGGAAGCAGCTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db      748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480 ACCCAC---GAATTTCAGAGGCGCCAGGAGTGTC 2512
Db      764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 12
ID      AAB66176
XX      AAB66176 standard; protein; 777 AA.
AC      AAB66176;
XX      02-APR-2001 (first entry)
XX      Protein of the invention #88.
XX      Secreted; transmembrane; gene therapy.
XX      Unidentified.
XX      WO200078961-A1.
XX      28-DEC-2000.
XX      18-FEB-2000; 2000WO-US004342.
XX      23-JUN-1999; 99US-0141037P.
XX      20-JUL-1999; 99US-0144758P.
XX      26-JUL-1999; 99US-0145698P.
XX      01-SEP-1999; 99WO-US020111.
XX      29-OCT-1999; 99US-0162506P.
XX      30-NOV-1999; 99WO-US028313.
XX      02-DEC-1999; 99WO-US028551.
XX      16-DEC-1999; 99WO-US030095.
XX      05-JAN-2000; 2000WO-US000219.
XX      06-JAN-2000; 2000WO-US000376.
XX      (GETH ) GENENTECH INC.
XX
XX      Baker KP, Boetstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX      Gao W, Goddard A, Godowski PJ, Grimaldi CU, Gurney AL, Hillan KJ;
XX      Pan J, Paoni NF, Roy WA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX      Williams PM, Wood WI;
XX      WPI; 2001-071395/08.
XX
XX      Secreted and transmembrane proteins and nucleic acids designated PRO,
XX      useful as hybridization probes, in chromosome and gene mapping and gene
XX      therapy.
XX
XX      Claim 1; Fig 176; 787pp; English.
XX
XX      The present invention relates to secreted and transmembrane proteins.
XX      These proteins and the DNA encoding them may be used as hybridization
XX      probes, in chromosome and gene mapping and in the generation of anti-
XX      sense RNA and DNA. They may also be used to generate either
XX      transgenic animals or knockout animals which are in turn useful for
XX      development and screening of therapeutically useful reagents. The nucleic
XX      acids may also be used in gene therapy

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SQ      Sequence 777 AA;
Alignment Scores:
Pred. No.: 7,75e-197 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.6% Conservative: 141
Best Local Similarity: 54.9% Mismatches: 177
Query Match: 45.8% Indels: 21
DB: 4 Gaps: 9
US-09-774-490-1 (1-2709) x AAB66176 (1-777)
QY      275 AAGACAATGTGCCAAGCGTGAATATATCTTACAAAGAAATTTTGAATCCAAATGTG 334
Db      39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY      335 ATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTTTTGGATGAGAA 394
Db      59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY      395 CGGAGTAGGCTGTATGTTGGAGCAAGGATCATATATTTTCATTCGACCTGTTAATATC 454
Db      79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY      455 ---AAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACAGAGAGATGAATCAAG 511
Db      99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
QY      512 TGGGCTGGAAGACATCTGAAAGATGTGCTAATTTTCATCAAGTACTTAAAGGCATAT 571
Db      119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY      572 AATCAGACTCACTTGTAGCCCTGTGGAACGGGGCTTTTTCATCCAAATTTGCACCTACAT 631
Db      139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY      632 GAAATTGACATCATCTCGAGGACAATATTTTTAAGTGGAGAACTCACATTTTGAAGAAC 691
Db      159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY      692 GCGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTATAGATGCA 751
Db      179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY      752 GAAATATATCTCTGGAACCTCGACTGATTTTATGGCGGAGACTTTGCTTCTTCCGAAT 811
Db      199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY      812 TTGGG-----CACCAACCAATCAGGACAGACGATGATTCCAGTGGCTC 862
Db      219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY      863 AATGATCCAAAGTTCATTAGTCCACCTCATCTCAGAGAGTGACAATCCCTGAAGATGAC 922
Db      239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY      923 AAAGTATATCTTTCTCCGTGAAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACT 982
Db      259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY      983 CACGCTAGATAGTTCAGATATGCAAGAAATGATTTTGGAGGCGCAGAGTCTGTGTAAT 1042
Db      279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
QY      1043 AAATGGACAACATTCCTCAAGCTGCTGTGTTTCTGCTCAGTCCGAGGTCCTCAATGCAT 1102
Db      299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY      1103 GACACTCAATTTTGTGAATCGAGGATGTATTTCCTAATGAACCTTTTAAAGATCCTAAAT 1162
Db      319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY      1163 CCAGTTGTATATGGAGTGTATTACGACTTCCAGTAACATTTTCAAGGATCAGCCGCTGT 1222

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Db      339  ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY      1223  ATGTATAGCATGAGTGTGAGAGGGTTCCTTGGTCCATATGCCACAGGGATGGA 1282
Db      359  ValTyrSerMetAlaAspIleAlaValPheAsnGlyProTyrAlaHisLysGlySer 378
QY      1283  CCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGGCAGCAACTCT 1342
Db      379  AlaAspHisArgTyrValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY      1343  CCAGCAAAACATTTGGTGTGTTTGAACCTTCAAAAGACCTTCTCGATGATGTTATA 1399
Db      399  ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
QY      1400  ACCTTTGCAAGAGTATCCAGCCATGATCAATCCAGTGTTCCTATGAAACATCCCCA 1459
Db      419  SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
QY      1460  ATAGTGATCAAAACGGATGTAAATTTATCAAAATTTGCTAGACCGAGTGGAT 1519
Db      439  ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY      1520  GCAGAGATGCAGCATGATGATGTTATGTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579
Db      459  AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY      1580  GTAGTTTCAATTCCTAAGAGACTGCTGATGATTTAGAGAGGTTCTGCTGGAAGATG 1639
Db      479  ValValSerIleSerLysGlyLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
QY      1640  ACAGTTTTCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCACAAAGCAGCAACA 1699
Db      498  GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGln 517
QY      1700  CTATATATTGTTCAACGGCTGGGTGCCAGTCCCTTTTACACCGGTGTGATTTTAC 1759
Db      518  LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY      1760  GGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGCTGGTGGATGGTCT 1819
Db      538  GlyLysAlaCysAlaAspCysLysLeuAlaArgAspProTyrCysAlaTyrAspGlyAsn 557
QY      1820  GCATGTTCTCGTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATATAAGAAAT 1879
Db      558  AlaCysSerArgTyrAlaProThrSerLysArgAlaArgAlaGlnAspValLysTyr 577
QY      1880  GGAGACCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
Db      578  GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY      1940  GAAGAGAGAAATCATCTATGCTGTAGAGATAGTACACATTTTGGATGAGTCCGAAG 1999
Db      597  AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY      2000  TGCAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
Db      617  SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY      2060  ATCAGAGTGGATGATCATATCATCAGGACAGTCAAGGCTTCTGCTAGTGTCTACAA 2119
Db      637  LeuLysProAspGluArgIleIleLysThrGlnTyrGlyLeuLeuIleArgSerLeuGln 656
QY      2120  CAGAAGGATTCAGGCAATTACCTCTGCCATCGGTGGAACTGGGTTCATCAAACTCTT 2179
Db      657  LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGlnHisThrPheIleHisThrIle 676
QY      2180  CTTAAGGTAAACCTGGAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCAATAAGAT 2239
Db      677  ValLysLeuThrLeuAsnValIleGluAsnGlnMetGluAsnThrGlnArgAlaGlu 696
QY      2240  GATGATGGAGTGGCTCTTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAG 2299

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Db      697  HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY      2300  GTCTGGTACAGACTTTCATGAGTCTATCAACCCCAATCTCAACACGATGGATGAG 2359
Db      711  LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY      2360  TTCTCTGACACAGTTTGGAAAGGACCGAAACAAACACGTCGCAAGAGCCAGCATACC 2419
Db      730  TyrCysGluGlnMetTyrHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY      2420  CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db      748  -----ProLysTyrIleHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480  ACCAC---GAATTTGAGAGGCGCCACCGAGGAGTGTCT 2512
Db      764  HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 13
AAU29197
ID  AAU29197 standard; protein; 777 AA.
XX
AC  AAU29197;
DT  18-DEC-2001 (first entry)
DE  Human PRO polypeptide sequence #174.
XX
KW  PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW  dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW  blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW  adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS  Homo sapiens.
XX
PN  WO200168848-A2.
XX
PD  20-SEP-2001.
XX
PF  28-FEB-2001; 2001WO-US006520.
XX
PR  01-MAR-2000; 2000WO-US005601.
PR  02-MAR-2000; 2000WO-US005841.
PR  03-MAR-2000; 2000US-0187202P.
PR  06-MAR-2000; 2000US-0186968P.
PR  14-MAR-2000; 2000US-0189320P.
PR  14-MAR-2000; 2000US-0189328P.
PR  15-MAR-2000; 2000WO-US006884.
PR  21-MAR-2000; 2000US-0190828P.
PR  21-MAR-2000; 2000US-0191007P.
PR  21-MAR-2000; 2000US-0191048P.
PR  21-MAR-2000; 2000US-0191314P.
PR  28-MAR-2000; 2000US-0192655P.
PR  29-MAR-2000; 2000US-0193032P.
PR  29-MAR-2000; 2000US-0193053P.
PR  30-MAR-2000; 2000WO-US008439.
PR  04-APR-2000; 2000US-0194449P.
PR  04-APR-2000; 2000US-0194647P.
PR  11-APR-2000; 2000US-0195975P.
PR  11-APR-2000; 2000US-0196000P.
PR  11-APR-2000; 2000US-0196187P.
PR  11-APR-2000; 2000US-0196690P.
PR  18-APR-2000; 2000US-0196820P.
PR  18-APR-2000; 2000US-0198121P.
PR  18-APR-2000; 2000US-0198585P.
PR  25-APR-2000; 2000US-0199397P.
PR  25-APR-2000; 2000US-0199550P.
PR  25-APR-2000; 2000US-0199654P.
PR  03-MAY-2000; 2000US-0201516P.
PR  17-MAY-2000; 2000WO-US013705.
PR  20-MAY-2000; 2000WO-US014042.
PR  30-MAY-2000; 2000WO-US014941.
PR  02-JUN-2000; 2000WO-US015264.

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PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 PI WPI; 2001-602746/68.
 DR N-PSDB; AAS46098.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 348; 774pp; English.
 XX Sequences AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 777 AA;
 SQ
 Alignment Scores:
 Pred. No.: 7.75e-197 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 4 Gaps: 9
 US-09-774-490-1 (1-2709) x AAU29197 (1-777)
 QY 275 AAGAACAAAGTGCCAGGCTGAAATATCTCAAAAGAAATGTTGGAATCCAAATG 334
 Db 39 LysGlnAsnIleProArgLeuLeuLeuLeuThrLysAspLeuLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCATGCTGGTGGCCACAGCTCCAGTTATCATACCTCTCTTTGGATGAGGAA 394
 Db 59 IleProLeuLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
 QY 395 CGAGTAGCTGTATGCTGAGCAAGAGATCATATTTTCATTCGACCTGGTTAATATC 454
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
 QY 455 ---AGGATTTTCAAGATTTGTCGCCAGTATCTTACACAGAGAGATGAATGCAAG 511
 Db 99 AsnLysAsnPhelLysIleTyrrPrpAlaLysGluArgValGluArgValGluCysLys 118
 QY 512 TGGGCTGGAAGAACATCTCCGAAAGAAATGTCATATTTTCATCAAGTACTTAAGGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138
 QY 572 AATCAGACTCATTTGTCGCCCTGTGGAAACGGGGCTTTTCATCCCAATTTGCACCTACATT 631
 Db

Db 139 AsnLysThrHisIleTyrrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
 QY 632 GAAATTTGGACATCATCTCCAGGACCAATATTTTTAAGCTGGAGAACTCACATTTTGAAC 691
 Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178
 QY 692 GGCCTGGAGAGTCCATATACCTTAAGCTGTCAGACAGATCCCTTTTAAATAGATGA 751
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 QY 752 GAAATTTACTCTGGAACTGCAGCTGATTTTATGGGCGAGACTTTGCTATCTTCCGAAC 811
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
 QY 812 CTTGGG-----CACCCACCACCAATCAGACAGACAGCAGCATGATTCAGGTGGCTC 862
 Db 219 LeuGlyProThrHisAspHisIleTyrrIleArgThrAspIleSerGluHisTyrrTrpLeu 238
 QY 863 AATGATCCAAAGTTCATTTAGTCCACCTCATCTCAGAGAGTGACATCTCGAAGATGAC 922
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrrAsnProAspAsp 258
 QY 923 AAGATATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACT 982
 Db 259 LysIleTyrPhePhePheArgGluSerGlnGluGlySerThrSerAspLysThrIle 278
 QY 983 CACGCTAGAATAGTGCAGATATCAGAAATGACTTTGGAGGCGCAGAGAGTCTGGTGAAT 1042
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
 QY 1043 AATGGACAAACTTCTCAAAGCTCGTCTGATTTGCTGAGTCCAGGTCCTCAATGTCATT 1102
 Db 299 LysTyrThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
 QY 1103 GACACTCATTTTGATGAAGTGCAGATGTATTCTTAATGAACTTTAAAGATCCTAAAT 1162
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrrLeuLeuProThrArgAspGluArg 338
 QY 1163 CCAGTTGTATATGGAGTGTTCACGACTTCCAGTAACATTTTCAAGGAGTACGCGGTGT 1222
 Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
 QY 1223 ATGTATAGCATGATGTGAGAGGGTGTCTTCTTGTTCATATGCCACAGGGATGA 1282
 Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
 QY 1283 CCCAACTATCAATGGTGCCTTATCAAGAGAGTCCCTATCCAGGCGCAGGAACTTCT 1342
 Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
 QY 1343 CCCAGCAAAACATTTTGGTGGT---TTTGACTCTCAAAAGGACCTTCTCTGATGATGATA 1399
 Db 399 ProSerLysThrTyrAspProLeuLeuLysSerThrArgAspPheProAspAspValIle 418
 QY 1400 ACCTTTGCAAGAGTATCCAGCCATGATCAATCCAGTGTCTTCTTCAATCAATCCCCCA 1459
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
 QY 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTACAAATTTGTCGTAGACCCAGTGGAT 1519
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
 QY 1520 GCAGAGATGACAGTATGATGTTATGTTATCGGAACAGATGTTGGGACCGTCTCTTAAA 1579
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 QY 1580 GTAGTTTCAATTTCTAAGAGACTTGGTATGATTTAGAGAGGTTCCTGCTGGAAGAAATG 1639
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeu 497
 QY 1640 ACAGTTTTCGGGAACCGCTCTATTTACAGCAATGAGACTTTCCACTGAGGAGCAACA 1699
 Db 498 GlnIlePheLysHisSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517

QY	1700	CTATATTGTTCAACGGTGGGGTTCGCCAGTCCCTTTTACACCGGTGTGATATTAC	1759	PN	US2003027272-A1.
Db	518	LeuTyrileGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537	XX	06-FEB-2003.
QY	1760	GGGAAACGCTGCTGAGTGTCTGCTGCGCCGAGACCTTACTGTCTGGGATGTTCT	1819	XX	21-JUN-2002; 2002US-00176492.
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn	557	PR	18-SEP-1997; 97US-0059263P.
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGACAGACGACAGATATAAAGAT	1879	PR	18-SEP-1997; 97US-0059266P.
Db	558	AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr	577	PR	17-OCT-1997; 97US-0062250P.
QY	1880	GGAGACCACTGACTCACTTCCAGACTTACCATGATAATCACCATGCCACACGCCCT	1939	PR	21-OCT-1997; 97US-0063486P.
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596	PR	24-OCT-1997; 97US-0063120P.
QY	1940	GAAGAGAGATCATCTATGTGTAGAGATAGTACACATTTTGGAAATGCCATGCCAAG	1999	PR	28-OCT-1997; 97US-0063540P.
Db	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616	PR	28-OCT-1997; 97US-0063541P.
QY	2000	TCCAGAGAGCGTGTCTTATTCGCAATCCAGAGCGGAAATCAAGAGCGAAAGAGAG	2059	PR	28-OCT-1997; 97US-0063544P.
Db	617	SerGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu	636	PR	29-OCT-1997; 97US-0063734P.
QY	2060	ATCAGAGTGGATGATCATATCATCAGCAGACAGATCAAGGCTTCTGCTAGTGTCTACAA	2119	PR	31-OCT-1997; 97US-0063870P.
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln	656	PR	31-OCT-1997; 97US-0064103P.
QY	2120	CAGAAAGATCAGCAATACCTCTGCGTGGTGGAGACATGGGTTCATACAAATCTTT	2179	PR	13-NOV-1997; 97US-0065311P.
Db	657	LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle	676	PR	21-NOV-1997; 97US-0066120P.
QY	2180	CTTAAGGTAACTCGAAGTCATTGACACAGACATTTGGAAGAACTTCTTCTATAAGAT	2239	PR	24-NOV-1997; 97US-0066466P.
Db	677	ValLysLeuThrLeuAsnValIleGluAsnGluMetGluAsnThrGlnArgAlaGlu	696	PR	24-NOV-1997; 97US-0066772P.
QY	2240	GATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG	2299	PR	11-DEC-1997; 97US-0069335P.
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710	PR	17-DEC-1997; 97US-0069870P.
QY	2300	GCTGTGTAGACAGATTCATGAGCTCATCAACCAACCCCAATCTCAACAGATGATGAG	2359	PR	18-DEC-1997; 97US-0068017P.
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729	PR	11-MAR-1998; 98US-0077632P.
QY	2360	TTCGTGTAAACAGTTTGGAAAGGACCGAAACAAACGTCGCAAGCGCAGGCATACC	2419	PR	11-MAR-1998; 98US-0077632P.
Db	730	TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly	747	PR	20-MAR-1998; 98US-0078886P.
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Alignment Scores:
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Score: 2245.50
Percent Similarity: 73.67%
Best Local Similarity: 54.92%
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DB: 21
Indels: 21
Gaps: 9

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GenCore version 5.1.1.6
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OM nucleic - protein search, using frame plus n2p model

Run on: March 8, 2005, 20:57:20 ; Search time 74 Seconds
(without alignments) 5465.522 Million cells

Title: US-09-774-490-1

Perfect score:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	%		DB	ID	Description
	Score	Match			
1	4201	85.8	771	1	US-08-121-713D-54
2	4201	85.8	771	1	US-08-835-268-54
3	4201	85.8	771	2	US-09-060-692-54
4	4201	85.8	771	3	US-08-833-391-54
5	4201	85.8	771	3	US-09-060-610-54
6	4201	85.8	771	5	PCT-US94-10151A-54
7	3568	72.9	655	4	US-08-556-422A-3
8	2562	52.3	477	1	US-08-136-922-2
9	2030	41.5	775	4	US-09-308-179B-1
10	1834	37.5	875	5	US-09-813-290-2
11	1830	37.4	782	4	US-09-813-290-4
12	982.5	20.1	862	4	US-08-556-422A-2

ALIGNMENTS

RESULT 1

US-08-121-713D-54
 ; Sequence 54, Application US/08121713D
 ; Patent No. 5639856
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/121,713D
 ; FILING DATE: 13-SEP-1993
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:

; INFORMATION FOR SEQ ID NO: 54:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-121-713D-54

Alignment Scores:

Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

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Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTTATCATACCTTC 379
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QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTGTGGACAAAGATCATATTTTCATTC 439
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QY 500 GATGAATCAAGTGGCTGGAAAGACATCTGGAAGATGTGCTAAATTCATCAAGTA 559
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QY 560 CTTAAGGCATATAATCAGACTCACTGTACCGCTGTGGAAACGGGGCTTTTCATCAATT 619
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QY 680 CATTTTGAAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
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QY 740 TTAATAGATGGAGAATTACTCTGGAACCTGACGCTGATTTTATGGGCGAGACTTGTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAACTCTTGGGCACACACCAATCAGACAGACAGCAGCATGATTCAGGTGG 859
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RESULT 2

US-08-835-268-54
; Sequence 54, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-835-268-54
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Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Db 741 ProGlyAsnSerAsnLysTyrLysHisLeuGlnLeuLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAAATTTAGAGGCGCCAGGAGGTCTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 3
US-09-060-692-54
; Sequence 54, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oeman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-692-54

Alignment Scores: 0 Length: 771
Pred. No.: 4201.00 Matches: 771
Score: 100.00% Conservative: 0
Percent Similarity:

Best Local Similarity: 100.00%		Mismatches: 0	
Query Match: 85.80%		Indels: 0	
DB: 2		Gaps: 0	
US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)			
QY	200	ATGGGCTGCTTAACTAGGATTGCTCTCTTTCTGGGAGTATTACTTTACAGCAAGACGA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACTATCAGAAATGGGAAGCAATGTGCAAGGCTGAAATTCCTACAAAGAAATGTTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCATACCTTC	379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTTGATGAGGAACGGAGTAGGCTGTATGTTGGACAAAGGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGTTTAATATCAAGGATTTTCAAAAGATTGTGTGCCAGATCTTTACACCAGAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGAATCAAGTGGCTGGAAAAAGACATCTCGAAAGAATGTCTAATTTTCATCAAGGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCATTTGTACGCTGTGGAACGGGGCTTTTCATCCAATT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATTTGAATTCGACATCATCTGAGGACAATATTTTAAGCTGGAGAACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGAGAATTATACTCTGGAACCTGCACTGATTTTATGGGCGAGACTTGTCT	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCGAACTCTTGGGACACCAACCCAAATCAGGACAGAGCATGATTCAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTTATTAGTGGCCCACTCATCTCAGAGAGTGACAACTCTGAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATACTTTTCTTCCTGAAATGCAATAGATGAGAAACACTCTTGAAAAAGCT	979
DB	241	AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGAAATAGGTACATATGCAAGATGACTTTGGAGGGGACAGAACTCTGGTG	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280
QY	1040	AATAAATGGACAACTTCCTCAAGCTCGTCTGATTTGCTCAGTGGCCAGGTCCTCAAAATGGC	1099
DB	281	AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTTCATCAACTGAGGATGTATTCCTAATGAACCTTTAAAGATCCTAAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATGAGAGTGTATACGACTTCAGTAACATTTTCAAGGATCAGCCGTG	1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340

QY	1220	TGTATGTATAGCATGAGTGAATCTGAGAAGGGTGTCTTCTTGGTCCATATATCCACAGGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCAACTATCAATGGGTGCTTATCAAGAAGAGTCCCTATCCAGGCGCAGAACT	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCACAGCAAACTTTGGTGGTGTGACTCTACAAAGGACCTTCTCATGATGTTATA	1399
DB	381	CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle	400
QY	1400	ACCTTTGCAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTATGAACATCCGCCA	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTATCAAAAACGGATGTAATATCAATTTACAAATTTGTCGTAGACCGAGTGGAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAAGATGACAGTATGATGTATTTATCGGAACAGATGTTGGGACCGTTCCTAAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	GTAGTTTCAATTTCTAAGGAGACTTGGTATGATTTTAGAAGAGGTCTCTGGAAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTCGGGAACCGACTCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln	500
QY	1700	CTATATATTGGTCAACGCTGGGTGCCAGCTCCCTTTACACGGGTGTATATTTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAGAGGTGTGCTGAGTGTGTGCTCGCCGAGAGCCCTTACTGTCTTGGATGTTCT	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAGATATAAGAAAT	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn	560
QY	1880	GGAGACCCACTGACTCTGTTACAGCTTACACCATGATTAATCACCATCGGCACACCCCT	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro	580
QY	1940	GAAGAGAGATCATCTATGTTGTAGAGATAGTACACATTTTGGAAATGCAAGTCCGAAG	1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys	600
QY	2000	TCGACAGAGACGCTCGTCTATTGGCAATTCAGAGCGCAAAATCAAGAGCAAAAGAGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTACTTACAA	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640
QY	2120	CAGAAGGATTTCAGGCAATTTACCTCTGCCATCGGTGGAAATCAATGGGTTTCATAAACTCT	2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu	660
QY	2180	CTTAAGGTAACCTCGAAGTCAATTCACACAGAGCAATTTGGAAGAACTTCTTCATAAGAT	2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp	680
QY	2240	GATGATGAGATGGCTCTNAGACCAAGAAATGTCCAATAGCATGACACTGACCCAGAGAG	2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys	700

QY 2300 GTCTGCTACAGACTTTCATGAGCTCATCAACCCCACTCAACAGGATGATGAG 2359
Db |||||
701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTTTGGAAAAGGACCGAAACCAACCTCGCGCAAGGCCAGGACATACC 2419
Db |||||
721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAATGGAGACCTTACAGAAAATAGAAAGGTAGAAACAGGAGG 2479
Db |||||
741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgarg 760
QY 2480 ACCCAGCAATTGAGAGGCGACCCAGGAGTGC 2512
Db |||||
761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4

US-08-833-391-54
; Sequence 54, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-391-54

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
Db: 3 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-833-391-54 (1-771)

QY 200 ATGGCTGTTTAACTAGGATTGTCTGCTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db |||||
1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGAAATGTTG 319
Db |||||
21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAACATGTGATCATTCTCAATGGCTTGCCACACAGCTCCAGTTATCATACCTTC 379
Db |||||
41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGAACGAGTAGGCTGTATCTGTGGACAAAGGATCACATATTTTCATTC 439
Db |||||
61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGA 499
Db |||||
81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgarg 100
QY 500 GATGAATGCAAGTGGCTGGAAAGACATCTGTAAGAAATGTCTTAATTTTCATCAAGTA 559
Db |||||
101 AspGluCysLysTrpAlaGlyLysAspLysLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCATTGTACGCCCTGTGGAACGGGGCTTTTCATCCAATT 619
Db |||||
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db |||||
141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACACGGCTGGGAAGAGTCCATATGACCTTACCTTAAGCTGCTCACAGCATCCCTT 739
Db |||||
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATATATCTCTGGAACTGCAGCTGATTTTATGGGCGAGACTTTCCT 799
Db |||||
181 LeuLeuAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAATCTTTGGGCACACACCCCAATCAGGACAGAGCATGATTCAGAGTGG 859
Db |||||
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTGACAACTCCTCAAGAT 919
Db |||||
221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979
Db |||||
241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTTCAGATATGCAAGAAATGACTTTTGGAGGCGACAGAGTCTGGTG 1039
Db |||||
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGCAACAATCTCTCAAAGCTCGTCTGATTCTCAGTCCAGGTCCTCAATGSC 1099
Db |||||
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGAATGAACTGCAGGATGTATTCTTAATGAATCTTAAAGATCCTAAA 1159
Db |||||
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGATATGAGAGTGTTCAGACTTCCAGTAATCTTCAAGGGATCAGCCGTG 1219
Db |||||
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGAGTGTGAGAAGGTTCTCTTGGTCCATATGCCCCACAGGAGT 1279
Db |||||
341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGCCTTTATCAAGGAAGAGTCCCTCTTACAGGCCAGGAAT 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTGGTGGTCTTCACTACAAAGGACCTTCCCTGATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY 1400 ACCTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACGAGTGAATTAATTCATTTACAAATTTCTGTAGACCGAGTGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 CGAGAAGATGGACAGTATGATGTTTATCGGAACAGATGTTGGGACCGCTTCTTAAA 1579
 Db 441 AlaGluAspGlyValnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
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 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTCGGAACCGACTCTATTTCCAGCAATGGAGCTTTCACCTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCACCGCTCGGGTTCGCCAGCTCCCTTTACACCGGTGCTATTTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GCGAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCCCTTACTGTGCTTGGGATGGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTCCCACTGCAAGAGACGCAAGAAGCAGCAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACCTGCTTACAGCTTACACCATGATTAATCACCATGGCCACAGCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGAAATCATCTGCTGATAGATAGTACATTTTGGATGCACTGCGAG 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGAGCCTGCTGCTATTTGGCAATTCAGAGCGCAAAATGAAGAGCAAAAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGATGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGGATTTCAGGCAATTCCTGCTCCATCGGTGGAACTGGTTCATACAACTCTT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGGTAAACCTGGAAGTCAATGACACAGACATTTGGAAGAACTTCTTCATAAGAT 2239
 Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAG 2299
 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCGTGACAGAGACTTCATGAGCTCATCAACCCCACTCAACACGATGATGAG 2359
 Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAGTTTGGAAAGGGACCGGAAACCAACGTCGGCAAGGCCAGCATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgArgGlnArgProGlyHisThr 740
 QY 2420 CCAGGGAACAGTAACAAATGGAAGCACCTTCAAGAAATAAGAAAGGTAGAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAAATTTAGAGGGCCACCCAGGAGTGTC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 5
 US-09-060-610-54
 ; Sequence 54, Application US/09060610
 ; Patent No. 6344544
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David R.
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,610
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION NUMBER: 08/835,268
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-060-610-54
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 3 Gaps: 0
 US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)
 QY 200 ATGGCTGTTAACTAGGATGTCTTTCTGGGAGTATTACTTACAGCAAGCA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAGAATGGGAAGCAATGTCCAGGCTGAAATTTATCTTACAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGGATAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTATATATCAAGATTTTCAAGATGTGTGGCCAGTATCTTACACAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATCAAGTGGCTGGAAAGACACATCTTGAAGATGTGCTAAATTTTCATCAAGTGA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAATTTGGACATCATCTGTAGGACAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAATATTACTCTGGAACTGCAGCTGATTTTATGGCGGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTCTTGGGACACACACCAATCAGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleLeuLeuThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGAGTGACAATCCTCAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTACTTTTTCTTCGCGTGAATGCAATAGATGGAGAACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGTAATAGTGCAGATATGCAAGATGATTTGGAGGCGCACAGATCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACAACTTCTCAAGCTCGTCTGATTGTCTCAGTCCAGGTCCAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGCAGAACTGCAGGATGTATTCCTAATGAACCTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCAGTTGTATATGAGTGTATAGACTTCCAGTAAACATTTTCAAGGATCAGCGGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGATCTGAGAAGGGTGTCTTGGTCCATATGCCCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGCTTATCAAGGAAGAGTCCCTATCCAGCGCCAGAACT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCAGCAACATTTGGTGGTTTGTACTACAAAGGACCTTCTGATGATCTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

QY 1400 ACCTTTGCAAGAAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTTATGAAACAATGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAATATCAATTTACAAATTTGCTGTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleValAspArgValAsp 440
QY 1520 GCAGAGATGACAGATGATGATGTTATCGGAACAGATGTTGGACCGTCTCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCCTCTCGAAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGGAAACCGACTGCTATTTTCAGAAATGGAGCTTTCACATAAGCAGACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTGCTTCAACGGCTGGGTTGCCCGAGACCCCTTACTGTGTCTGGGATGGTTCT 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCGTGTGCTGAGTGTTCCTCCCGAGACCCCTTACTGTGTCTGGGATGGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGTATTTTCCCACTGCAAGAGACGCAACAGCAGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCACTGACTCAGTGTTCAGACTTACACATGATATACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAAGAGAAATCATCTAGTGTAGAGAAATAGTAGCACATTTTGGAAATGCAAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGCAATTAAGAGCGCAAAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCCTTCTGCTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATCGGTGGAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGGAAGTCAATTGACACAGAGCAATTTGGAAGAATCTTCTTCATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATCAGACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTTCATGCGCTCATCAACCCCACTTCCTCAACACGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAACTTTGGAAGGACCGAAAAACACGTCGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAACAGGAG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCGAGAAATTTGAGAGGAGCACCAGGAGTGC 2512
 Db |||||||
 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 6
 PCT-US94-10151A-54
 ; Sequence 54, Application PC/TUS9410151A
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR HOEBACH TEST ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/10151A
 ; FILING DATE: 13-SEP-1994
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299 FHT UR
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 PCT-US94-10151A-54

Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

QY 200 ATGGGCTGTTAACTAGGATGTTCTCTTTCTGGGAGTATTACTTACAGCAAGCA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAAGTGGGAAGCAATGTGCCAAGCTGAAATTTATCTACAAAGAAATGTTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCCAAATGTGATCTCTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATGAGAAACGGAGTAGGCTGTATGTTGGAGCAAGATCACATATTTTCATTC 439
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGTTAATATCAAGATTTTCAAAAGATTGTGGCCAGTATCTTACACCAAGCA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnIleValTrpProValSerTyrThrArgArg 100

QY 500 GATGAATGCAAGTGGCTGGAAAAAGACATCTCTGAAAGAAATGCTTAATTTTCATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCAGCTTGTACGCTGTGGAAACGGGGCTTTTCATCCAAAT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTGAAATTTGGACATCATCTCTGAGCACAATATTATTTTAAGCTGGAGACTCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTAAAAACGGCGCTGGGAAGAGTCCATATGACCCCTAACTGCTGTCAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAAGAAATTAATCTCTGAACTGCAGCTGATTTTATGGGGGAGACTTTGCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCCGAACCTCTTTGGGCACCACCACCAATCAGGACAGACAGCATGATTCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCATGATCCTCAAGTTCATTAGTCCACCTCATCTCAGAGAGTGCACATCTCTGAAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGAACACTCTGAAAAGCT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTTAGAATAGGTCAGATATGCAAGAAATGACTTTTGGAGGGCACAAGATCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGGAACAATCTCTCAAGCTGCTCTGATTTGCTAGTCCAGGTCAAAATGGC 1099
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 QY 1100 ATTGACACTCATTTTGGTCACTGAGGATGATTCTTAATCAACTTTAAAGATCTCTAAA 1159
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 QY 1160 AATCCAGTTGTATATGAGTGTTTTACGACTTCAGTAACTTTTCAAGGGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGAGTATGTAGAGGGTGTCTTCTGGTCCATATGCCACACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCAACTATCAATGGTGGCTTTTCAAGGAAGAGTCCCTATCCAGCCGAGCAACT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGCTCCAGCAAAACATTTGGTGGTGTGTTTACTTACAAAGAGCTTCTCTCATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAAGAGTATCCAGCCATGATCAATCCAGTGTTCCTTCTATGAACAATCCCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGTCAAAACCGATGTAATTAATTCATTTTACAAATTTGCTGAGACCGAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAGAGTGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGCTTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAGAGGTTCTCTGGAAGAAATG 1639

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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556.422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

QY 200 ATGGCTGTTAACTAGGATTGCTCTTTCTGGGGAGTATTACTTACAGCAAGACA 259
DB 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGGCTGAAATATCTCAAAAGAAATGTTG 319
DB 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATATGATCATCTTTTCAATGGCTTGGCCACAGCTCCAGTATCATACCTTC 379
DB 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCATTC 439
DB 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGA 499
DB 81 AspLeuValAsnIleLysAspPheGlnLysIleValTyrProValSerTyrThrArg 100
QY 500 GATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCTCAAGTA 559
DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCAGCTTGTACGCTGTGGAAACGGGGCTTTTTCATCAAT 619
DB 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
DB 141 CysThrTyrIleGluIleGlyHisIleProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGCATCCCTTT 739
DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTAATCTCTGAACTGACGCTGATTTTATGGGGGAGACTTTGCT 799
DB 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTTGGGCACCCACCAATCAGGACAGACAGACAGATGATTCAGAGTGG 859
DB 201 IlePheArgThrLeuGlyHisIleHisIleProIleArgThrGluGlnHisAspSerArgTyr 220
QY 860 CTCATATGATCCAAAGTTTATTTAGTCCCACTCATCTCTGAGAGTGCACATCTCTGAGAT 919
DB 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATCTTTTCTTCCTCGTGAATGCAATAGATGGAGAACACCTCTCGAAAAGCT 979
DB 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

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RESULT 7

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US-08-556-422A-3
; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSETIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.

```

QY 980 ACTACGCTAGAAATAGTATGCAAGATGACTTTGGAGGGGACAGAAAGTCTGGNG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGACAACTCTCAAGAGTCTGCTGATTTGCTCAGTGCAGGTCCAAATGCG 1099
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCAATTTGATGAAGTGCAGGATGATTTCTTAATGAACCTTTAAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelLysAspProLys 320
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 Db 341 CysMetTySerMetSerAspValArgValPheLeuGlyProTyzAlaHisArgAsp 360
 QY 1280 GGACCAACTATCAATGGTGGCTTTATCAAGGAAGAGTCCCTATCCAGCGCCAGAACT 1339
 Db 361 GlyProAsnTyzGlnTrpValProTyzGlnGlyArgValProTyzProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGACTCTCAAGAGGACCTTCCTGATGATGTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAAGAGTCATCCGCCATGTACATCCAGTGTTCCTATGAACATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyzAsnProValPheProMetAsnAsnArgPro 420
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 Db 421 IleValIleLysThrAspValAsnTyzGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 CGAAGATGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyzAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 TGATGTTCAATTCCTAAGAGACTGGTATGATTTAGAGAGGTTCCTGCGAAGATG 1639
 Db 461 ValValSerIleProLysGlnThrTrpTyzAspLeuGluValLeuLeuGluGluMet 480
 QY 1640 ACAGTTTTTCGGGAACCGACTGCTATTTCCAGCAATGGAGCTTTCCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGTTCAACGGCTCGGGTTCGCCAGTCCCTTTACACCGGTGTGATATTAC 1759
 Db 501 LeuTyzIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyz 520
 QY 1760 GGAAGAGCGTGTGCTGAGTGTTCCTCGCCGAGACCCCTTACTGCTGGATGGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyzCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGACGACCAAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyzPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCCACTGCTGCTTTCAGACTTTACACCATGATTAATCACCATGGCCACGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisPheAsnHisPheGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTGGATTCGAGTCCGAG 1999
 Db 581 GluGluArgIleIleTyzGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGCCGCTGCTCTATTGGCAATTCAGAGCGCAATTAAGAGCGAAAGAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyzTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620

QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTACAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGGATTACAGCAATTTACCTGCTCCATGCGGTGGAACATGGG 2164
 Db 641 GlnLysAspSerGlyAsnTyzLeuCysHisAlaValGluHisGly 655

RESULT 8
 US-08-136-922-2
 ; Sequence 2, Application US/08136922
 ; Patent No. 5416197
 ; GENERAL INFORMATION:
 ; APPLICANT: Raper, Jonathan A.
 ; APPLICANT: Luo, Yuling
 ; TITLE OF INVENTION: Compositions Which Regulate Neural
 ; TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ; ADDRESSEE: No. 5416197ris
 ; STREET: One Liberty Place
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/136,922
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deluca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: UPN-1428
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 477 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-136-922-2

Alignment Scores:
 Pred. No.: 3,46e-246 Length: 477
 Score: 2562.00 Matches: 472
 Percent Similarity: 99.37% Conservative: 0
 Best Local Similarity: 99.37% Mismatches: 3
 Query Match: 52.33% Indels: 0
 DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-136-922-2 (1-477)

QY 899 GAGAGTGAATCTCGAAGATGACAAAGTATATCTTTCTCCGCGAATAATGCAATAGAT 958
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 QY 959 GGAGAACACTCTGGAAAGCTACTCACCTAGAATAGTTCAGATATGCAAGATGACTTT 1018
 Db 22 GlyGluHisSerGlyLysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPhe 41
 QY 1019 GGAGGGCAGACAGAGTCTGTTGAATAAATGGACAAATTCCTCAAGCTCGTCTGATTTGC 1078
 Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrThrPheLeuLysAlaArgLeuLysCys 61
 QY 1079 TCAGTGCCAGGTCCAAATGGCACTTTCATTTTGTGATGAACACTGACAGGATGATTCCTTA 1138

Db 147 ValGlyHisSerGluGluProLeuPheHisLeuGluSerHisArgSerGluArgGly 166
QY 695 CGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGAGAA 754
Db 167 ArgGlyArgCysProPheAspProAsnSerSerPheValSerThrLeuValGlyAsnGlu 186
QY 755 TTATACTCTGGAACTCGACTGATTTTATGATGGGCGAGACTTGTCTATCTTCGAACTCTT 814
Db 187 LeuPheAlaGlyLeuTyrSerAspTyrTrpGlyArgSerAlaIlePheArgSerMet 206
QY 815 GGGCACCACCACCAATCAGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAG 874
Db 207 GlyLeuGlyHisIleArgThrGluHisAspAspGluArgLeuLeuGlyGluProLys 226
QY 875 TTCATTAGTGGCCACCTCATCTCAGAGAGTGACAACTCCTGAAGATGACAAAGTATATCTT 934
Db 227 PheValGlySerTyrMetIleProAspAsnGluAspArgAspAsnLysMetTyrPhe 246
QY 935 TTCTTCGGTGAATGCATAGATGGAGAACACTCTGGAAAGCTACTCAGCGTAGAATA 994
Db 247 PhePheThrGluLysAlaLeuGluAlaGluAsnAsnAlaHisThrIleTyrThrArgVal 266
QY 995 GCTCAGATATGCAAGATGACATTGAGGGCCACAGAGTCTGGTGAATAAATGGCAACA 1054
Db 267 GlyArgLeuCysValAsnAspMetGlyGlyGlnArgIleLeuValAsnLysTrpSerThr 286
QY 1055 TTCTCAAAAGCTGCTGATTTGCTCAGTGCCAGGTCCAAATGGCAATTCACACTCATTTT 1114
Db 287 PheLeuLysAlaArgLeuValCysSerValProGlyMetAsnGlyIleAspThrTyrPhe 306
QY 1115 GATGAATCAGAGATGATTTCTTAATGAATTTAAAGATCCCTAAAAATCCAGTTGATAT 1174
Db 307 AspGluLeuGluAspValPheLeuLeuProThrArgAspProLysAsnProValIlePhe 326
QY 1175 GGAGTCTTACGACTTCCAGTAACATTTTCAAGGATACCGCTGTATGTATGATACCATG 1234
Db 327 GlyLeuPheAsnThrThrSerAsnIlePheArgGlyHisAlaValCysValTyrHisMet 346
QY 1235 AGTGATGTGAGAGGGTGTCTTGGTCCATATGCCACAGGATGAGCCCAACTATCAA 1294
Db 347 SerSerIleArgGluAlaPheAsnGlyProTyrAlaHisLysGluGlyProGluTyrHis 366
QY 1295 TGGGTGCTTATCAAGAAAGTCCCTATCCACGCCAGGAACTTGTCCCGCAAAACA 1354
Db 367 TrpSerLeuTyrGluGlyLysValProTyrProArgProGlySerCysAlaSerLysVal 386
QY 1355 TTGTGGTGT---TTTGACTCTCAAAAGGACCTTCTGTATGATGATTAACCTTTGCAAGA 1411
Db 387 AsnGlyGlyLysTyrGlyThrThrLysAspTyrProAspAspAlaIleArgPheAlaArg 406
QY 1412 AGTCATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATGCCCAATAGTATCAA 1471
Db 407 MetHisProLeuMetTyrGlnProIleLysProValHisLysLysProIleLeuValLys 426
QY 1472 ACGGATGTAATTAATCAATTTTACAAATTTGCTAGACCGAGTGGATGAGAGATGGA 1531
Db 427 ThrAspGlyLysTyrAsnLeuArgGlnLeuAlaValAspArgValGluAlaGluAspGly 446
QY 1532 CAGTATGATGTTATGTTTATCGGAACAGATGTTGGACCGCTTCTTAAAGTAGTTTCAAT 1591
Db 447 GlnTyrAspValLeuPheIleGlyThrAspThrGlyIleValLeuLysValIleThrIle 466
QY 1592 CCTAAGGAGACTTGGTATGATTTAGAGAGTTCCTGCGAAGAATGACAGTTTTCGG 1651
Db 467 TyrAsnGlnGluThrGluTrpMetGluGluValIleLeuGluGluLeuGlnIlePheLys 486
QY 1652 GAACGACTGCTATTTCCAGCAATGAGGCTTCCACTAAGCAGCAACAATATATATGTT 1711
Db 487 AspProAlaProIleSerMetGluIleSerSerLysArgGlnLeuTyrIleGly 506
QY 1712 TCAACGGCTGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTTACGGGAAGCGTGT 1771
Db 507 SerAlaSerAlaValAlaGlnValArgPheHisCysAspMetTyrGlySerAlaCys 526

QY 1772 GCTGAGTGTGCTCCTCGCCGAGACCCCTTACTGTCTGCTTGGATGGTTCGATGTTCTCC 1831
Db 527 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyIleSerCysSerArg 546
QY 1832 TATTTTCCCACT-----CCTAAGAGACCCACAGACGACAGATATAGAATGGA 1882
Db 547 TyrTyrProThrGlyAlaHisAlaLysArgArgPheArgGlnAspValArgHisGly 566
QY 1883 GACCCACTGACTCACTGTTTCAGACTTACACCATGATTAATCACCATGGCCACACCCCTGAA 1942
Db 567 AsnAlaAlaGlnGlnCysPheGlyGlnPheValGlyAspAlaLeuAspArgThrGlu 586
QY 1943 GAGAGAAATCATCTATGTTGAGAGTATAGTACACATTTTGGAAATGCGAGTCCG 2002
Db 587 GluArgLeuAlaTyrGlyIleGluSerAsnSerThrLeuLeuGluCysThrProArgSer 606
QY 2003 CAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGCAATGAAGAGCGGAAAGAGATC 2062
Db 607 LeuGlnAlaLysValIleTrpPheValGlnLysGlyArgAspValArgLysGluGluVal 626
QY 2063 AGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTCTAGTAGTCTACACAG 2122
Db 627 LysThrAspAspArgValValLysMetAspLeuGlyLeuLeuPheLeuArgValArgLys 646
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Db 745 -----SerProSerLysTrpLysTyrAlaAsnProGlnGluLys---Arg 758
QY 2471 AACAGGAGGACCCAGCAATTTGAGAGGCGCCACCCAGG 2506
Db 759 LeuArgSerLysAlaGluHisPheArgLeuProArg 770

RESULT 10

US-09-813-290-2
; Sequence 2, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodi
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22

; PRIOR APPLICATION NUMBER: US 60/193,639
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 875
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-09-813-290-2

Alignment Scores:
 Pred. No.: 1.66e-173 Length: 875
 Score: 1834.00 Matches: 379
 Percent Similarity: 62.24% Conservative: 150
 Best Local Similarity: 44.59% Mismatches: 261
 Query Match: 37.46% Indels: 60
 DB: 4 Gaps: 16

US-09-774-490-1 (1-2709) x US-09-813-290-2 (1-875)

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QY	144	CGG-----CACAAATACA	155
DB	63	ProGlyGlySerArgAlaAsnTyrAsnArgArgProAlaGlyProGluGlyGlySerAla	82
QY	156	GGAAGAGACTTAAGCAGCAAGGACCTACA---GGCTGTCAGCATGGCTGGTTAA	212
DB	83	GlyArgGlnArgCysProGlnPheProSerMetAlaProSerAlaTrpAla-Ile--	101
QY	213	CTAGGATGTCGTCTTTCTGGGAGATTACTTACCAAGAGCAAACTATCAGATG	272
DB	102	-----Cys- TrpLeuLeuGlyGlyLeuLeuLeuHisGlySerSerGlyProSerP	119
QY	273	GGAAGAACAAATGCGCAAGCTGAAATATCTACAAAGAAATGTTGGAATCCAACAATG	332
DB	119	roGlyProSerValProArgLeuArgLeuSerTyrArgAspLeuLeuSerAlaAsnArgS	139
QY	333	TGATCATCTTCAATGGCTGGCCACAGCTCCAGTTATCATACCTTCCTTTGGATGAGG	392
DB	139	erAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAlaMetTyrLeuAspGluT	159
QY	393	AACGAGTAGGTGATGTTGGACCAAGAGTACATATTTTCATTCGACCTGGTTAATA	452
DB	159	yrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSerLeuArgLeuAspGlnA	179
QY	453	TC---AAGGATTTTCAAAAAGATTGTGGCCAGTATCTTTACACCAAGAGATGAATGCA	509
DB	179	laTrpProAspProArgGluValLeuTrpProGlnProGlyGlnArgGluGlyCysV	199
QY	510	AGTGGCTGGAAGACATCTCGAAGATGTCGTAATTTTCATCAAGGTACTTAAGCAT	569
DB	199	alArgLysGlyArgAspProLeuThrGluCysAlaAsnPheValArgValLeuGlnProH	219
QY	570	ATAATCAGACTCACTTGTACGCTGGGAACGGGGCTTTTCATCCAAATTTGCACCTACA	629
DB	219	isAsnThrHisLeuLeuAlaCysGlyThrGlyAlaPheGlnProThrCysAlaLeuI	239
QY	630	TTGAAATGGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCACATTTTGAAA	689
DB	239	leThrValGlyHisArgGlyGlu---HisValLeuHisLeuGluProGlySerValGluS	258
QY	690	AGCGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGATCCCTTTTAATAGATG	749
DB	258	erGlyArgGlyArgCysProHisGluProSerArgProPheAlaSerThrPheIleAspG	278
QY	750	GAGAATTACTCTGGAACCTGAGCTGATTTTATGGGGGAGACTTTTGTCTATCTCCGAA	809
DB	278	lyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIlePheArgS	298
QY	810	CTCTTGGGCACCACCAATCAGGACAGCAGCATGATTCAGGTGGCTCAATGATC	869

DB	298	erGlyGlyProArgProAlaLeuArgSerAspSer---AspGlnSerLeuLeuHisAspP	317
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DB	317	roArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAsnAspLysValT	337
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DB	376	ysTrpSerThrPheLeuLysAlaArgLeuValCysSerValProGlyGlyAlaG	396
QY	1104	ACACTCATTTGATGAACACTGCAGGATGATTCTTAATGAACCTTTAAAGATCCTAAAAATC	1163
DB	396	luThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGlyLysSerL	416
QY	1164	CAGTTGATATGAGTGTATTAGACTTCCAGTACATTTTCAAGGGATCAGCCGTGTGA	1223
DB	416	euGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCysV	436
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DB	496	luValLeuGlnPheAlaAlaGlnHisProLeuMetPheTrpProValArgProArgHisG	516
QY	1452	ATCGCCCAATAGTGTCAAAACGGATGTAATAATTTATCAATAATTTGCTAGTACCC	1511
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DB	536	rgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThrAspSerGlySerV	556
QY	1572	TTCCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTGTAAGAGAGTTCTGCTGG	1631
DB	556	alLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluProGluGluValValLeuG	576
QY	1632	AAGAAATGACAGTCTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGGCTTTCCACTAAGC	1691
DB	576	luGluLeuGlnValPheLysValProThrProIleThrGluMetGluIleSerValLysA	596
QY	1692	AGCAACAATATATATTTGTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGGTGTG	1751
DB	596	rgLnmMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCysG	616
QY	1752	ATATTTTACGGGAACCGTGTGCTGAGTGTGTGCTCGCCGAGACCTTACTGTGCTGGTGG	1811
DB	616	luThrTyrGlyThrAlaCysAlaGluCysLeuAlaArgAspProTyrCysAlaTrpA	636
QY	1812	ATGTTCTGCAATTTCTCGCTATTTTCCACT---GCAAGAGACGCAACAGACGACAAG	1868
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QY	1869	ATATGAAGAAATGGAGACCCACTGACTCTGTTTACAGATTACCATGATATCATCATG	1928

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Db 656 spIleArgHisGlyAsnProAlaLeuGlnCysLeu-----G 668
QY 1929 GCCACAGCCCTGAAGAGAGA-----ATCATCTATGGTGTAG 1964
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QY 1965 AGAATAGTAGCATTATTTGGAAATGAGTCGCGAAGTCGAGAGAGCGCTGGTCTATWGGC 2024
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QY 2427 ACAGTAACAATGGAAGCACTTACAGAAATAAGAAAGGTAGAACAGGAGGCCAGC 2486
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RESULT 11
US-09-813-290-4
; Sequence 4, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 782
; TYPE: PRT
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; ORGANISM: homo sapiens
US-09-813-290-4

Alignment Scores:
Pred. No.: 3,91e-173 Length: 782
Score: 1030.00 Matches: 366
Percent Similarity: 64.17% Conservative: 139
Best Local Similarity: 46.51% Mismatches: 244
Query Match: 37.38% Indels: 38
DB: 4 Gaps: 13

US-09-774-490-1 (1-2709) x US-09-813-290-4 (1-782)
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Db 28 ProSerValProArgLeuArgLeuSerTyArgAspLeuLeuSerAlaAsnArgSerAla 47
QY 338 ACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATATACCTCTCTTTTGGATGAGAACGG 397
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QY 398 AGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTTCATTCGACCTGGTTAATATC--- 454
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 QY 701 AAGAGTCCATATGACCTAAGCTGTCACAGCATCTCTTTTAAATAGATGAGAAATATATAC 760
 Db 155 ArgCysProPheAspProAlaHisSerTyrThrSerValMetValAspGlyGluLeuTyr 174
 QY 761 TCTGNACTGACGCTGATTTTATGGGCGAGACTTTGCTATCTTCCGAACCTCTTGGGCAC 820
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 QY 881 AGTGCCCATCTCATCTCAGAGACT---GACATCTCT-----GAAGATCAAAAGTATAC 931
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 QY 932 TTTTCTTCCGCGAAATGCAATAGATGAGAGAACTCTGGAAGACTACTCAGCGTAGA 991
 Db 233 PhePhePheThrGluValSerValGluTyrGluPheValPheArgValLeuIleProArg 252
 QY 992 ATAGTGCATATGCAAGATGACTTTTGAGGCGCAGAGACTGCTGTGTAATAAGTACGA 1051
 Db 253 IleAlaArgValCysLysGlyAspGlnGlyLeuArgThrLeuGlnLysLysIleTrpThr 272
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 Db 273 SerPheLeuLysAlaArgLeuIleCysSerArgProAspSerGlyLeuVal----- 289
 QY 1112 TTGTATGAATCAGGATGATTTCTTAATGAATCTTAAAGATCTTAAAGATCCAGTTGTA 1171
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 QY 1232 ATGAGTGTGTGAGAGGTGTTCCTT---GGTCCATATGCCACAGG-----GAT 1279
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 Db 350 GlnSerHisThrLysIleValArgTyrAsnGlyProValProLysProArgProGlyAla 369
 QY 1340 TGT-----CCAGCAAAACATTTGGTGTGTGTGACTCTACAAAGAGCTTCTGTATGAT 1393
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 QY 1394 GTTATACTTTGCAAGAAGTATCCAGCATGCTCAATCCAGTGTTCCTATGACAAT 1453
 Db 390 ThrLeuGlnPheValLysAspHisProLeuMetAspSerValThrProIleAspAsn 409
 QY 1454 CGCCCAATATGATCAAAACGGATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1513
 Db 410 ArgProArgLeuIleLysLysAspValAsnTyr-----ThrGlnIleValValAspArg 427
 QY 1514 GTGGATGCAAGATCGACAG---TATGATGTATCTTTATCGGAACAGATGTGGGAC 1570
 Db 428 ThrGlnAlaLeuAspGlySerValTyrAspValMetPheValSerThrAspArgGlyAla 447

QY 1571 GTTCTTAAGTAGTATTTTCAATTCCTAAGGAGACTTGGTATGATTTTAAAGAGGTT----- 1624
 Db 448 LeuHisLysAlaIleSer-----LeuGluHisAlaValHis 459
 QY 1625 CTGCTGGAGAAATGACAGTCTTTTCGGGAACCGACTGCTGCTATTTTACCAATGAGGTTTCC 1684
 Db 460 IleIleGluGluThrGlnLeuPheGlnAspPheGluProValGlnThrLeuLeuLeuSer 479
 QY 1685 ACTAAGCAG-----CAACAATATATATTTGCTTCAACCGCTGGGTTTCCCGAGTCTCCCT 1738
 Db 480 SerLysLysGlyAsnArgPheValTyrAlaGlySerAsnSerGlyValGlnAlaPro 499
 QY 1739 TTACACCGGTGTGATATTTACCGGAAAGCGTGTGCTGAGTGTGCTCCCGCAGACCTT 1798
 Db 500 LeuAlaPheCysGlyLysHisGly---ThrCysGluAspCysValLeuAlaArgAspPro 518
 QY 1799 TACTCTGCTTGG-----TACTCTGCTTGG-----TACTCTGCTTGG----- 1810
 Db 519 TyrCysAlaTrpSerProProThrAlaThrCysValAlaLeuHisGlnThrGluSerPro 538
 QY 1811 -----GATGGTCTTCGCTATGCTTCTCGCTATTTTCCCT 1840
 Db 539 SerArgGlyLeuIleGlnGluMetSerGlyAspAlaSerValCys-----Pro 554
 QY 1841 ACTGCAAGAGACGCAAGACGACAGCAAGATATAGAAATGGAGACCCACTGACTCTGT 1900
 Db 555 AspLysSerLysGlySerTyrArgGln----- 563
 QY 1901 TCAGACTTACCATGATTAATCACCATGCCACAGCCCTGGAAGAGAGATCATCTATGTT 1960
 Db 564 -----HisPhePheLysHisGlyGlyThrAlaGlu----- 573
 QY 1961 GTAGAGAATAGTAGCACATTTTGGAAATGCACTCCGAACTCCAGAGCGCTGGTCTAT 2020
 Db 574 -----LeuLysCysSerGlnLysSerAsnLeuAlaArgValPhe 586
 QY 2021 TGGCAATTCAGAGCGGAAATGAAGCGGAAAGAGAGATCAGAGTGGATGATCATATC 2080
 Db 587 TrpLysPheGln-----AsnGlyValLeuLysAlaGlu-----SerProLysTyrGly 602
 QY 2081 ATCAGACAGATCAAGCGCTTCTGCTAGTACTTCAACAAGAGATTTTCAAGCAATTTAC 2140
 Db 603 LeuMetGlyArgLysAsnLeuLeuIlePheAsnLeuSerGluGlyAspSerGlyValTyr 622
 QY 2141 CTCTCCATCGGTGCAACATGGTTCATACAACTCTTCTTAAAGTA----- 2188
 Db 623 GlnCysLeuSerGluGluArgValLysAsnLysThrValPheGlnValValAlaLysHis 642
 QY 2189 -----ACCTGGAAGTCAATTGAC 2206
 Db 643 ValLeuGluValLysValValProLysProValValAlaProThrLeuSerValValGln 662
 QY 2207 ACAGAG 2212
 Db 663 ThrGlu 664

RESULT 13

US-09-854-845-29
 ; Sequence 29, Application US/09854845
 ; Patent No. 6750054
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wang, Xiaoming
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6750054e1 Human Semaphorin Homologs and Polynucleotides Enco
 ; FILE REFERENCE: LEX-0177-USA
 ; CURRENT APPLICATION NUMBER: US/09/854,845
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 60/205,274
 ; PRIOR FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: US 60/208,893

287	CAAGGCTGAATTATCTTACAAAGAATGTTGGAATCCAAACAATGTGATCACTTTCAAT	346
QY		
34	ProArgMetThrIleProTyrGluGluLeuSerGlyThrArgHis	50
Db		
347	GCCTGGCCAAACAGCTCCAGTATCATACCTTCCTTTGGATGAGGACGAGTAGGCTG	406
QY		
51	GlyGlnAla-----GlnAsnTyrSerThrLeuLeuLeuGluGluAlaSerAlaArgLeu	68
Db		
407	TATGTTGGAGCAAAAGCATCACATATTTTCATCTTCACCTGGTAAATCAAGGAT-----	460
QY		
69	LeuValGlyAlaArgGlyAlaLeuPheSerLeuSerAlaAsnAspIleGlyAspGlyAla	88
Db		
461	TTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAAGATGAATGCAAGTGGCTGGA	520
QY		
89	HisLysGluIleHisIleTrpGluAlaSerProGluMetGlnSerLysCysHisGlnLysGly	108
Db		
521	AAAGACATCCTGAAAGAATGTCTTAATTTTCATCAAGTACTTAAAGCATATATCAAGCT	580
QY		
109	LysAsnAsnGlnThrGluCysPheAsnHisValArgPheLeuGlnArgLeuAsnSerThr	128
Db		
581	CACTTGTACGCTGTGGAAACGGGGCTTTTCATCCAATTTGACCTACATTTGAAATGGA	640
QY		
129	HisLeuTyrAlaCysGlyThrHisAlaPheGlnProLeuCysAlaIleLeuAla----	147
Db		
641	CATCATCCTGTGGAGACAATATTTTAAAGCTGGAGAACTCACATTTTGAACCGCCGTGG	700
QY		
148	-----GluAlaPheThrLeuProThrSer--PheGluGluGlyLysGlu	161
Db		
701	AAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAATAGATGGAGAATTATAC	760
QY		
162	LysCysProTyrAspProAlaArgGlyPheThrGlyLeuIleIleAspGlyGlyLeuTyr	181
Db		
761	TCGTGAAGTCGACGCTGATTTTATGGGCGAGACTTTCGTATCTTCGAACTCTTGGGCAC	820
QY		
182	ThrAlaThrArgTyrGluPhe-----ArgSerIleProAspIleArgSerArgHis	199
Db		
821	CACCACCCAATCAGACAGACAGCATGATTTCCAGTGGCTCAATGATCCAAAGTTTCAT	880
QY		
200	ProHisSerLeuArgThrGluGluThrProMetHisIleProLeuAsnAspAlaGluPheVal	219
Db		
881	AGTGCCCACTCATCTCAGAGAGTGACAAATCCT-----GAAGATGACAAAGTATAC	931
QY		
220	PheSerValLeuValArgGluSerLysAlaSerAlaValGlyAspAspIleLysValTyr	239
Db		
932	TTTTTCTCCGGAATGCAATAGATGGAGAACACTCTCTGMAAGCGTACTCAC-----	985
QY		
240	TyrPhePheThrGluArgAlaThrGlu----GluGlySerGlySerPheThrGlnSerArg	258
Db		
986	-----GCTAGAATAGGTCCAGATATGCAAGTAAATGACTTTTGGAGGGCCACAGA	1031
QY		
259	SerSerHisArgValAlaArgValAlaArgValCysLysGlyAspLeuGlyLysLys	278
Db		
1031	AGTCTGGTGAATAAATGGACAAATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGT	1091
QY		


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Db 523 ProTyrCysGlyTyrAspProGlyThrHisAlaCysAlaAlaThrThrThrIleAlaAsn 542
QY 1850 AGACGCACAGCAGCAAGATATAAGAAATGAGAGCCCACTGACTGCTTTCAGACTTA 1909
Db 543 ArgThrAlaLeuIleGlnAspIleGluArgGlyAsn-----ArgGlyCys 557
QY 1910 CACCATGATAATCACCATGGCCACAGCCCTGAAGAGAGATCATCTATGGTGTAGAGAAT 1969
Db 558 GluSerSerArgAspThrGlyProProProProLeuLeuYsThrArgSerValLeuArgGly 577
QY 1970 AGTAGACACATTTTGAATGCGAGTCGGAAGTCGAGAGCCCTGCTATTTGG-----2023
Db 578 AspAspValLeuLeuProCysAspGlnProSerAsnLeuAlaArgAlaLeuTrpLeuLeu 597
QY 2024 -----CAATTCAGAGCGGAATGAAGAGCGCAAGAGAGATCAGAGTGGATGATCAT 2077
Db 598 AsnGlySerMetGlyLeuSerAspGlyGlnGlyGlyTyrArgValGlyValAsp-----615
QY 2078 ATCATCAGGACAGATCAAGCCCTTCTGCTACGCTAGTCTACACAGAGAGATTCAGGCAAT 2137
Db 616 -----GlyLeuLeuValThrAspAlaGlnProGluHisSerGlyAsn 629
QY 2138 TACCTCTGCCATCGGTGGAACATCGGTTCATACAACTCTTCTT 2182
Db 630 TyrGlyCysTyrAlaGluGluAsnGly---LeuArgThrLeuLeu 643

RESULT 15
US-09-854-845-27
; Sequence 27, Application US/09854845
; Patent No. 6750054
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wang, Xiaoming
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6750054el Human Semaphorin Homologs and Polynucleotides Encod
; FILE REFERENCE: LEX-0177-USA
; CURRENT APPLICATION NUMBER: US/09/854,845
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/205,274
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/208,893
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 843
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-854-845-27

Alignment Scores:
Pred. No.: 3,44e-83 Length: 843
Score: 927.50 Matches: 230
Percent Similarity: 50.15% Conservative: 101
Best Local Similarity: 34.85% Mismatches: 256
Query Match: 18.94% Indels: 73
DB: 4 Gaps: 23

US-09-774-490-1 (1-2709) x US-09-854-845-27 (1-843)
QY 287 CCAAGGCTGAATTTATCTTACAAAGAAATGTTGGAATCCAAACATGTGATCATCTTCAAT 346
Db 34 ProArgMetThrIleProTyrGluGluLeuSerGlyThrArgHis-----Phelys 50
QY 347 GCGTGGCCCAACAGCTCCAGTATCATACCTTCTTGGATGAGGAGGAGGAGGAGGAGGAGG 406
Db 51 GlyGlnAla-----GlnAsnTyrSerThrLeuLeuGluGluAlaSerAlaArgLeu 68
QY 407 TATGTTGGAGCAAGGATCACATATTTTCATTCGACCTCGTGTAAATATCAAGAT-----460
Db 69 LeuValGlyAlaArgGlyAlaLeuPheSerLeuSerAlaAsnAspIleGlyAspGlyAla 88

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QY 461 TTTCAAAGATTGTGGCCAGTATCTTACACACAGAGAGATGAATGCAAGTGGCTGGA 520
Db 89 HisLysGluIleHisIleTrpGluAlaSerProGluMetGlnSerLysCysHisGlnLysGly 108
QY 521 AAAGACATCTCGAAGAAGATGCTAAATTTTCATCAAGGTACTTAAGGCATATATCAGACT 580
Db 109 LysAsnAsnGlnThrGluCysPheAsnHisValArgPheLeuGlnArgLeuAsnSerThr 128
QY 581 CACTTGTACGCTGTGGAACCGGGCTTTTCATCCAAATTTGCACCTACATCAAAATTTGGA 640
Db 129 HisLeuTyrAlaCysGlyThrHisAlaPheGlnProLeuCysAlaAlaIleAspAla---147
QY 641 CATCATCTGAGGACAATATTTTAAAGCTGAGAACTCACATTTTGAACCGCGCTGG 700
Db 148 -----GluAlaPheThrLeuProThrSer---PheGluGluGlyLysGlu 161
QY 701 AAGAGTCCATATGACCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGGAATATATAC 760
Db 162 LysCysProTyrAspProAlaArgGlyPheThrGlyLeuIleIleAspGlyGlyLeuTyr 181
QY 761 TCTGNACTGCGAGCTGATTTTATGGGCGCAGACTTTGTCTATCTTCCGAACTCTTGGGCA 820
Db 182 ThrAlaThrArgTyrGluPhe-----ArgSerIleProAspIleArgSerArgHis 199
QY 821 CACCACCAATCAGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCAAT 880
Db 200 ProHisSerLeuArgThrGluThrProMetHisTrpLeuAsnAspAlaGluPheVal 219
QY 881 AGTGGCCACCTCATCTCAGAGAGTGCACATCT-----GAAGATGACAAAGTATAC 931
Db 220 PheSerValLeuValArgGluSerLysAlaSerAlaValGlyAspAspLysValTyr 239
QY 932 TTTTCTTCTCGTAAATGCAATAGATGGAACACACTCTGGAAGAGTACTCAC-----985
Db 240 TyrPhePheThrGluArgAlaThrGlu---GluGlySerGlySerPheThrGlnSerArg 258
QY 986 -----GCTAGAATAGTGCAGATATGCAAGATGATCTTCTTAAATGAACCTTAA 1150
Db 259 SerSerHisArgValAlaArgValCysLysGlyAspLysGlyGlyLysLys 278
QY 1031 AGTCTGGTGAATTAATGGAACAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGT 1090
Db 279 IleLeuGlnLysLysTrpThrSerPheLeuLysAlaArgLeuIleCysHisIlePro---297
QY 1091 CCAATGGCATTTGACACTCATTTTGAATGCAACTGACAGAGTATCTTCTTAAATGAAC 1150
Db 298 -----LeuTyrGlnThrLeuArgGlyValCysSerLeuAspAlaGlu 311
QY 1151 GATCTTAAATCCAGTTGTATATGAGAGTGTTCAGCTTCCAGT-----AACATTTTC 1204
Db 312 ThrSerSerArgThrHisPheTyrAlaAlaPheThrLeuSerThrGlnTrpLysThrLeu 331
QY 1205 AAGGATCAGCGTGTGTATGATAGCATGATGATGAGAGGCTGCTCTTCTGCTCA 1264
Db 332 GluAlaSerAlaIleCysArgTyrAspLeuAlaGluIleGlnAlaValPheAlaGlyPro 351
QY 1265 TATGCCACAGGATGAGCCCAACTATCAATGGGTGCTTATCAAGGAGAGTCCCTAT 1324
Db 352 TyrMetGluTyrGlnAspGlySerArgArgTrpGlyArgTyrGluGlyValProGlu 371
QY 1325 CCACGGCAGGAACCTTGT-----CCAGCAAAACATTTGGTGGTTGACTCTCAAG 1378
Db 372 ProArgProGlySerCysIleThrAspSerLeuArgSerGlnGlyTyrAsnSerSerGln 391
QY 1379 GACTTCTGATGATTTATAACCTTTCGAAGAGTATCCAGCATGTACAAATCCAGTG 1438
Db 392 AspLeuProSerLeuValLeuAspPheValLysLeuHisProLeuMetAlaArgProVal 411
QY 1439 TTTCTATCAACAATCGCCCAATAGTATCAAAACGGATGTAATATCAATTTTACAA 1498
Db 412 ValProThrArgGlyArgProLeuLeuLysArgAsnIleArgTyr-----ThrHis 429
QY 1499 ATTGCTGAGACCGAGTGCAGAGATGGA-----CAGTATGATGTTATGTTTTCGGA 1555

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Db	430	LeuThrGlyThrProValThrThrProAlaGlyProThrTyrAspLeuLeuPheLeuGly	449
Qy	1556	ACGATGTTGGGACCGTTCTAAAGTAGTTTCAATTCTCAAGGAGACTTGGTATGATTTA	1615
Db	450	ThrAlaAspGlyTrpIleHisLeuAlaValValLeuGlySerGlyMetHis	466
Qy	1616	GAAGAGTTCTGCTGGGAAGAAATACAGAGTTTTTCGGAAACCGACTGCTATTTTCAGCAATG	1675
Db	467	-----IleIleGluGluThrGlnValPheArgGluSerGlnSerValGluAsnLeu	483
Qy	1676	GAGCTTTCCTAAGCAGCAACAACATATATATGTTCAACGGCTGGGTGGCCAGCTC	1735
Db	484	ValIleSerLeuLeuGlnHisSerLeuTyrValGlyAlaProSerGlyValIleGlnLeu	503
Qy	1736	CTTTTACACCGGTGTGATATTTACGGGAAAGCGTGTCTCAGTGTTCCTCGCCCGGAGAC	1795
Db	504	ProLeuSerSerCysSerArgTyr--ArgSerCysTyrAspCysIleLeuAlaArgAsp	522
Qy	1796	CTTTACTGTGCTGGGATGGTTCT-----GCATGTCTCGCTATTTTCCACTGCAAAAG	1849
Db	523	ProTyrCysGlyTrpAspProGlyThrHisAlaCysAlaAlaThrThrIleAlaAsn	542
Qy	1850	AGA-----CCACACAGACGA---CAAGATATAGAATCGAGACCCACTGACT	1894
Db	543	ArgSerGlnGlySerArgThrAlaLeuIleGlnAspIleGluArgGlyAsn-----	559
Qy	1895	CACTGTTTCAGACTTACACCATGATATACCATCGGCCACACCGCTCAAGAGAGAAATCATC	1954
Db	560	-----ArgGlyCysGluSerSerArgAspThrGlyProProProLeuLeuThrArg	577
Qy	1955	TATGGTGTAGAAATAGTAGACATTTTTCGGAATGCAGTCCGAGTGCAGAGAGCGCTG	2014
Db	578	SerValLeuArgGlyAspAspValLeuLeuProCysAspGlnProSerAsnLeuAlaArg	597
Qy	2015	GTCTATTGG-----CAATTCAGAGCGGAAATCAAGCGCGMAAAGAAGAGATC	2062
Db	598	AlaLeuTrpLeuLeuAsnGlySerMetGlyLeuSerAspGlyGlnGlyTyrArgVal	617
Qy	2063	AGAGTGGTGATCATCATCATCAGACAGATCAAGGCCCTTCGTGATCGTAGCTACACAG	2122
Db	618	GlyValAsp-----GlyLeuLeuValThrAspAlaGlnPro	629
Qy	2123	AAGATTACGGCAATTAACCTCTGCCATCGCGTGGACATCGGTTTCATACAACTCTTCTT	2182
Db	630	GluHisSerGlyAsnTyrGlyCysTyrAlaGluAsnGly---LeuArgThrLeuLeu	648

Search completed: March 8, 2005, 21:42:01
Job time : 151 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 8, 2005, 20:46:14 ; Search time 92.5 Seconds
(without alignments)
5635.702 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896

Sequence: 1 aatcttttatttcatgatg.....aggctttttttcttaataacc 2709

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2.1/USPTO spool_p/US09774490/runat_08032005_140758_14848/app.query.fasta_1.2887
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LCOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09774490 @CNC 1 1 138 @runat_08032005_140758_14848 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	2	D49423 semaphorin III pre
2	3989.5	81.5	772	2	I48747 semaphorin D - mou
3	3784.5	77.3	772	2	A49069 collapsin - chicke
4	3478.5	71.0	666	2	I58169 semaphorin III - m
5	2118	43.3	749	2	G01856 semaphorin V - hum
6	2059.5	42.1	748	2	I48744 semaphorin A - mou
7	1952	39.9	753	2	G02173 semaphorin III fam
8	1850.5	37.8	751	2	I48748 semaphorin E - mou
9	966	19.7	834	2	S66498 M-sema F protein p
10	857.5	17.5	782	2	I48746 semaphorin C - mou
11	828	16.9	1011	2	JC8059 semaphorin 6D-1 -
12	802	16.4	760	2	I48745 semaphorin B - mou
13	785.5	16.0	724	2	C49423 semaphorin II prec
14	766.5	15.7	730	2	JH0798 fasciclin IV precu

15	731.5	14.9	656	2	B49423 semaphorin I - fru
16	730	14.9	1074	2	JC5928 semaphorin F precu
17	699.5	14.3	712	2	T27165 hypothetical prote
18	684.5	14.0	711	2	A49423 semaphorin I precu
19	534	10.9	653	2	T03102 semaphorin homolog
20	327	6.7	676	2	T33853 hypothetical prote
21	197	4.0	1894	2	JC4980 plexin 1 precursor
22	188.5	3.9	1945	2	TJ3937 plexin A - fruit f
23	186	3.8	1872	2	JC4976 plexin 3 precursor
24	184	3.8	441	2	S29921 hypothetical prote
25	180	3.7	403	2	E42521 A39r protein - vac
26	172	3.5	1884	2	JC4975 plexin 2 precursor
27	170	3.5	1905	2	I51553 Plexin - African c
28	167	3.4	2051	2	TJ3164 plexin B - fruit f
29	154.5	3.2	1568	2	T09074 semaphorin recepto
30	134.5	2.7	1806	2	T23298 hypothetical prote
31	127.5	2.6	295	2	J01775 sail9r protein - v
32	123	2.5	573	1	CSBYT catalase [EC 1.11.
33	120	2.5	904	2	S3896 DNA mismatch repai
34	119	2.4	1104	1	A36866 microbial collagen
35	118.5	2.4	1291	2	T09273 probable tail-host
36	118.5	2.4	1654	2	A12067 two-component sens
37	118	2.4	1379	1	S01254 hepatocyte growth
38	117.5	2.4	1029	2	H86179 hypothetical prote
39	115	2.3	3381	2	T42389 versican precursor
40	114.5	2.3	993	2	A36873 protein-tyrosine k
41	114	2.3	692	1	S57592 probable phosphoe
42	113	2.3	1276	2	T09204 probable tail-host
43	112.5	2.3	248	2	A46652 glucosamine-6-phos
44	112	2.3	4273	2	C59679 polyketide synthas
45	111.5	2.3	6642	2	T29757 protein UNC-89 - C

ALIGNMENTS

RESULT 1

D49423

semaphorin III precursor - human

C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: D49423

R:Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.

Cell 75, 1389-1399, 1993

A:Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone

A:Reference number: A49423; MUID:94094332; PMID:8269517

A:Accession: D49423

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-771 <KOL>

C:Genetics:

A:Gene: GDB:SEMA1

A:Cross-references: GDB:283448

C:Superfamily: semaphorin

Alignment Scores:

Pred. No.:	1.39e-309	Length:	771
Score:	4201.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	85.80%	Indels:	0
DB:	2	Gaps:	0

US-09-774-490-1 (1-2709) x D49423 (1-771)

QY : 200 ATGGCTGGTTAACTAGGATTGCTCTTTCTGGGGAGTATTACTTACAGCAGACGA 259

|||||

Db 1 MetGlyTrpLeuThrArgileValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

|||||

QY 260 AACTATCATGATGGCAGACAAATGTCACAGGCTGAAATTCCTACAAAGAAATGTTG 319

|||||

Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40

|||||

320 GAATCCAAATGATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTC 379
41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
380 CTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAACATATTTTCATTC 439
61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
440 GACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGTAGTATCTTACACCAAGA 499
81 AspLeuValAsnIleLysAspPheGlnIlylleValTrpProValSerTyrThrArg 100
500 GATGAATGCAAGTGGCTGCAAAAGACATCTCTGAAGAATGTCTTAATTCATCAAGTGA 559
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
560 CTTAAGGCATATANTCAGACTCATTGTAGCGCTGTGNAACGGGGCTTTTCATCAATTT 619
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
620 TGCACCTACATTAATGGACATCATCTGTAGGACATATATTTTAAAGCTGGAGAACTCA 679
141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
680 CATTTTGAACCGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTT 739
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
740 TTAATAGATGGAATATATCTGTGAAGTGTGAGTATTTTATGGGGGAGACTTTGCT 799
181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
800 ATCTTCCGAACCTTGGGCACACACCACTCATGAGACAGACAGATGATTCAGAGTGG 859
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
860 CTCAATGATPCCAAAGTTCAATAGTGCACCTCATCTCAGAGAGTCAATCTCTGAAGAT 919
221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
920 GACAAATGATATCTTTTCTCGTGAAATGCAATAGATGGAGACACTCTGGAAAGCT 979
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
980 ACTCAGCTAGATAGTGCAGATATGCAAGATGATTTGGAGGACAGAGAGTCTGGTG 1039
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
1040 AATAAATGGACAACTTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGC 1099
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
1100 ATTGACACTCATTTGATGAAGTGCAGGATGATTCCTTAATGAACCTTAAAGATCTTAAA 1159
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
1160 AATCCAGTTGATATGGAGTGTATACGACTTCAGTAAACATTTTCAAGGATCAGCCGTG 1219
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
1220 TGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATCCACACAGGAT 1279
341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
1280 GGACCCCACTATCAATGGGTGCTTATCAAGGAGAGTCCCTATCCACGGCCAGAACT 1339
361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
1340 TGTCCCAAGCAAACTTTCGTGGTTTGAATCTTCAAAAGGACTTCTCATGATGTTATA 1399
381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
1400 ACCTTTGCAAGAAGTATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAATCGCCA 1459

401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
1460 ATAGTGATCAAAACGGATGTAATTTATCAAAATTTGTCTAGACCGAGTGGAT 1519
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
1520 GCAGAGATGACAGTATGATGTTATCGGAACAGAGATGTTGGACCGTCTTTAAA 1579
441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
1580 GTAGTTTCAATTCCTAAGGAGACTTGTATGATTTAGAGAGGTCTCTCTGGAAGAAATG 1639
461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCACATAAGCAGCAACA 1699
481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
1700 CTATATATTGTTCAACGGCTGGGTTGCCAGAGTCCCTTTTACACCGGTGTGATATTTAC 1759
501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
1760 GGGAAAGCGTGTGCTGAGTGTTCCTCCCGAGACCTTACTGTCTTGGATCGTCT 1819
521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATATAAGAAAT 1879
541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
1880 GGAGACCACTGACTCACTGTTTACAGACTTACACCATGATAATCACCATGGCCACACCT 1939
561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
1940 GAAGAGAAATCATCTGTTGTAGAGAAATAGTAGACATTTTGGAAATGCACTCCGAAG 1999
581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
2000 TCGCAGAGAGCGCTGCTTATTGGCAATTCAGAGCGCAAAATGAAGAGCAAAAGAG 2059
601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620
2060 ATCAGATGCGATGATCATATCATCAGGACAGATCAAGCGCTTCTGCTACGTAGTACAA 2119
621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
2120 CAGAAGGATTCAGGCAATTTACTCTGCCATGCGGTGGAAACATGGGTTTATCAAACTCTT 2179
641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
2180 CTTAAGGTAAACCTCGAAGTCAATTCACACAGAGCATTTGGAAGAACTTCTTCAAAAGAT 2239
661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
2240 GATGATGAGATGGCTCTAAGACCAAAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
2300 GTCTGTTACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACAGATGATGAG 2359
701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
2360 TTCTCTGTAACAGTTTGGAAAGGACCGAAACAACTCGGCAAGGCGCAGACATACC 2419
721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAAAATAAGAAAGGTGAACACGAGG 2479
741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
2480 ACCCAAGAAATTTGAGAGGCGCACCCAGGAGTGTCT 2512


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Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 2
148747
semaphorin D - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48747
R:Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
A:Reference number: I48744; MUID:95267431; PMID:7748561
A:Accession: I48747
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-772 <RES>
A:Cross-references: UNIPROT:008665; EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g8543
C:Genetics:
A:Gene: semD
C:Superfamily: semaphorin
Alignment Scores:
Pred. No.: 1,38e-293 Length: 772
Score: 3989.50 Matches: 730
Percent Similarity: 97.28% Conservative: 21
Best Local Similarity: 94.56% Mismatches: 20
Query Match: 81.48% Indels: 1
DB: 2 Gaps: 1
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QY 260 AACTATCAAAATGGGAGAACATGTGCCAAGCTGAATTTATCTTACAAAGAAATGTG 319
Db 21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCATCCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACCGGATGAGTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGATTTTCAAAGATTTGTGCGCCAGTATCTTACACCGAAGA 499
Db 81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGGCTGGAAGAAGACATCCTGAAGAAGATGCTAATTTTCATCAAGT 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCATTGTACGCTGTGGAAACGGGGCTTTTCATCAATTC 619
Db 121 LeuGluAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAAATTCGATCATCATCTGAGGACAAATATTTTAAGCTGAGAACTCA 679
Db 141 CysThrTyrIleGluValGlyHisProGluAspAsnIlePheLysLeuGlnAspSer 160
QY 680 CATTTTGAACGGCGTGGGAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAAATTACTCTGAACTGACAGCTGATTTTATGGGGGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAACTCTTGGGCACCAACCAATCAGGACAGAGCAGCATGATTCAGGTTGG 859
Db 201 IlePheArgThrLeuGlyAspHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGATTCATTTAGTCCCACTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
Db 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240
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QY 1100 ATTGACACTCATTTTGTGATGAACTGCAGGATGTATTCCTTAATCACTTTTAAGATCCATA 1159
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QY 1160 AATCCAGTTGTATATGGAGTGTTTACGACTTCAGTAAACATTTCAAGGATCAGCCGTG 1219
Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGATGAGAAGGGTTCCTTGGTCCATATCCACACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCGCAGGAAT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGCTCCACAAACATTTGGTGGTTCCTCTACAAAGAGCTTCCTCTGATGATGTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTGCAAGAAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACATCCCCA 1459
Db 401 ThrPheGlyArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArgPro 420
QY 1460 ATAGTATCAAAACCGATGTAATATCAATTTACAAATTTGCTGTAGACCGAGTGGAT 1519
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QY 1520 GCAGAGATGGACATGATGATGTTATCGGAACAGATGTTGGGACCGCTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAGAGGTCTCTGCGAAGAAATG 1639
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QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTTCCTCAAGCAGCAACA 1699
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QY 1700 CTATATATTTGGTTCAACGGCTGGGTTCGCCAGCTCCCTTTACCGGTGTGATTTTAC 1759
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QY 1760 GGAAGAGCTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTCTGGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCACAAAGACGACCAAGATATAAGAAAT 1879
Db 541 SerCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGATCTGATCTGTTTACAGCTTACAC---CATGATAATCACCATGCCACAGC 1936
Db 561 GlyAspProLeuThrHisCysSerAspLeuGluAspHisAspAsnHisIleGlyProSer 580
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Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspGluValIle 400
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QY 1460 ATAGTCATCAAAACGATGTAATATCAATTTACAAATTTGTCTAGACCGAGTGGAT 1519
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QY 1520 GCAGAGATGACAGATGATGATGTTATGTTATCGGAACAGATGTTGGGACCGTCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspIleGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATCTTAAGAGACTTGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpHisGluLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTAGCAATGAGCTTCCACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrValIleSerAlaMetLysIleSerThrLysGlnGlnGln 500
QY 1700 CTATATATTGTTCAACGGTGGGGTGCACGCTCCCTTTACACCGGTGTATATTAC 1759
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QY 1760 GGGAAACGCTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTTTGGATGTTCT 1819
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Db 541 SerCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCAGTTCAGACTTA--CACCATGATAATCACCATGCCACAGC 1936
Db 561 GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnProSerGlyGlnThr 580
QY 1937 CCTGAAGAGAGAAATCATCTATGTTGAGAGATAGTAGACATATTTTGAATGCATCGC 1996
Db 581 LeuGluGluLysIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 600
QY 1997 AGTCCGACAGAGCGCTGTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAA 2056
Db 601 LysSerGlnArgAlaIleValTyrTrpGlnPheGlnLysGlnAsnAspHisLysVal 620
QY 2057 GAGTCAGAGTGGATCATATCATCAGACAGATCAAGCGCTTCTGCTAGTAGTCTA 2116
Db 621 GluIleLysValAspAspArgMetIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu 640
QY 2117 CAACAGAAGGATTCAGCGCAATACCTCTGCGATGCGGTGGAACATGGGTTCATACAACT 2176
Db 641 GlnArgArgAspSerGlyIleTyrPheCysHisAlaValGluHisGlyPheIleGlnThr 660
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QY 2237 GATGATGAGGATGGCTCTAAGACCAAGAAATGTCCTCAATAGCATGACCTAGCCAG 2296
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Db 721 GluPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProAlaAsn 740
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QY 2477 AGGACCCAGAAATTTGAGAGGCGACCCAGAGTGTCT 2512
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RESULT 4

semaphorin III - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
R:Accession: I58169
R:Messemersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.; K.
Neuron 14, 949-959, 1995
A:Title: Semaphorin III can function as a selective chemorepellent to pattern sensory p.
A:Reference number: I58169; MUID:95267432; PMID:7748562
A:Accession: I58169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-666 <RES>
A:Cross-references: UNIPROT:008665; GB:I40484; NID:G703189; PIDN:AAA73934.1; PID:G70319
C:Genetics:
A:Gene: SemIII
C:Superfamily: semaphorin

Alignment Scores:
Pred. No.: 6,04e-255 Length: 666
Score: 3478.50 Matches: 633
Percent Similarity: 98.50% Conservative: 23
Best Local Similarity: 95.05% Mismatches: 9
Query Match: 71.05% Indels: 1
DB: 2 Gaps: 1

US-09-774-490-1 (1-2709) x I58169 (1-666)

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QY 578 ACTCACTGTGTAGCCCTGTGGAACGGGGCTTTTTCATCAATTTGCACCTACATTTGAAAT 637
Db 21 ThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIleCysThrTyrIleGluVal 40
QY 638 GACATCATCTCTGAGACAAATATTTTAAGCTGGAGAACATCATATTGGAACGCCCGT 697
Db 41 GlyHisHisProGluAspAsnIlePheLysLeuGlnAspSerHisPheGluAsnGlyArg 60
QY 698 GGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAAATAGATGAGAAATTA 757
Db 61 GlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeuLeuIleAspGlyGluLeu 80
QY 758 TACTCTGGAACCTGACAGCTGATTTTATGGGCGAGACTTTTGTCTATCTTCCGAACCTCTGGG 817
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 Db 401 AlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyrGlyLysAlaCysAlaGlu 420
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 Db 461 CysSerAspLeuGlnHisHisAspAsnHisHisGlyProSerLeuGluGluArgIleIle 480
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 QY 2495 AGGCGACCCAGGAGTGTC 2512
 Db 661 ArgAlaProArgSerVal 666
 RESULT 5
 G01856
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 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C:Accession: G01856
 R:Sekido, Y.
 submitted to the EMBL Data Library, June 1995
 A:Reference number: G08634
 A:Accession: G01856
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-749 <SEK>
 A:Cross-references: UNIPROT:Q13214; EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g9742
 C:Superfamily: semaphorin
 Alignment Scores:
 Pred. No.: 4,95e-152 Length: 749
 Score: 2118.00 Matches: 404
 Percent Similarity: 67.22% Conservative: 123
 Best Local Similarity: 51.53% Mismatches: 185
 Query Match: 43.26% Indels: 72
 DB: 2 Gaps: 12
 US-09-774-490-1 (1-2709) x G01856 (1-749)
 QY 221 GTCTGCTTTTCTGGGAGTATTACTTACAGACAGCAAACTATCAGATGGGAAGAAC 280
 Db 13 LeuAlaLeuLeuTrpAlaValGlyLeuGlySerAlaAla-----Pro 26
 QY 281 AATGTGCCAAGGCTGAAATTTATCTTACAAAGAAATGTTGGAATCCAAATGTGTACT 340
 Db 27 SerProProArgLeuArgLeuSerPheGlnGluLeuGlnAlaTrpHisGlyLeuGlnThr 46
 QY 341 TTCATGCTGGCCCAACAGCTCCAGTTATCATACCTTCCTTCCTTGGATGAGAACGGAGT 400
 Db 47 PheSer---LeuGluArgThrCysCysTyrGlnAlaLeuLeuValAspGluGluArgGly 65
 QY 401 AGGCTGTATGTGGAGCAAGATCATATTTTCATTCGACCTCGTTTAATATC---AAG 457
 Db 66 ArgLeuPheValGlyAlaGluAsnHisValAlaSerLeuAsnLeuAspAsnIleSerLys 85
 QY 458 GATTTTCAAAAGATGTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGT 517
 Db 86 ArgAlaLysLysLeuAlaTrpProAlaProValGluTrpArgGluGluCysAsnTrpAla 105
 QY 518 GGAAAGACATCTCGAAAGATGTGCTAATTTTCATCAAGTACTTAAGCATATATCAG 577
 Db 106 GlyLysAspIleGlyThrThrGluCysMetAsnPheValLysLeuLeuHisAlaTyrAsnArg 125

Qy	578	ACTCAC	TTGTAC	CGCCTGT	GAAACGGGG	CTTTTC	TATCCAA	TTTGC	ACTTAC	ATTGAA	ATT	637	
Db	126	ThrHis	LeuLeu	AlaCys	GlyThr	GlyAla	PheHis	ProThr	CysAla	PheVal	GluVal	145	
Qy	638	GGACAT	CATCCT	CAGGACA	TATTTT	TAAGCT	CGAGAAC	TCCAC	ATTTTGGAA	ACGCCGT	697		
Db	146	GlyHis	ArgAla	GluGlu	ProVal	LeuArg	LeuAsp	ProGly	ArgIle	GluAsp	GlyLeu	165	
Qy	698	GGGAAG	AGTCCAT	ATAGAC	CCCTTA	AGCTCT	CACAGCA	TCCCTTTT	TAATAG	ATGAGAGA	ATTAA	757	
Db	166	GlyLys	SerPro	TyrAsp	ProArg	HisArg	AlaAla	SerVal	LeuVal	GlyGlu	LeuLeu	185	
Qy	758	TACTCT	GGAACT	GCAGCT	GTATTT	TATGGG	GGGAGAC	TTTCTG	CTATCT	TCTTCC	GAAC	CTCTTGGG	817
Db	186	TyrSer	GlyVal	AlaAla	AspLeu	MetGly	ArgAsp	PheThr	IlePhe	ArgSer	LeuGly	205	
Qy	818	CACCAC	CACCA	CAATC	ACGAC	GACGAC	GCATG	ATTCC	AGGTGG	CTCAAT	GATCCAA	AGTTTC	877
Db	206	GlnArg	ProSer	IleThr	GluPro	HisAsp	SerArg	TrpLeu	AsnGlu	ProLys	Phe	225	
Qy	878	ATTAGT	CCCCAC	CTCAT	CTCAG	AGAGT	GACAA	TCTCTG	AAGAT	GACAA	AGATAT	ACTTTTTT	937
Db	226	ValLys	ValPhe	ThrIle	ProGlu	SerGlu	AsnPro	AspAsp	LysIle	TyrPhe	Phe	245	
Qy	938	TTCCGT	GAAATG	CAATAG	ATGG	AGACAC	TCT---	GGAA	AGCTACT	CAGCTAG	ATA	994	
Db	246	PheArg	GluThr	AlaVal	GluAla	AlaPro	AlaLeu	GlyArg	LeuSer	ValSer	ArgVal	265	
Qy	995	GGTCAG	ATATG	CAAGA	TGACTT	TGGAG	GGCAC	AGAAG	TCTGGT	TGAATA	AAATCG	CAACA	1054
Db	266	GlyGln	IleCys	ArgAsn	AspVal	GlyGly	GlnArg	SerLeu	ValAsn	LysTrp	ThrThr	285	
Qy	1055	TTCTCA	AAAGCT	CGCTCT	GATTG	CTCAG	TGCC	AGGTCCA	ATGG	CAATGG	CACTG	ACTATTTT	1114
Db	286	PheLeu	LysAla	ArgLeu	ValCys	SerVal	ProGly	ValGlu	Gly---	AspThr	HisPhe	304	
Qy	1115	GATCA	ACTGC	AGGATG	TATTC	TCTTA	TCAACT	TAA	GATCCT	TAAAT	CAGCTG	TGTATAT	1174
Db	305	AspGln	IleuGln	AspVal	PheLeu	LeuSer	SerArg	HisPhe	Sarg	ThrPro	LeuLeu	Tyr	324
Qy	1175	GGAGT	GTTTAC	GACTTC	CAGTAA	CAATTTT	CAAGG	GATC	AGCGTGT	GTATGT	ATAG	CATG	

RESULT 6

RESOUR
I48744

140/44
semaphorin A - mouse

C:Species: Mus musculus (house mouse)

C/species: Mus musculus (house mouse)
C/date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 09-Jul-2004

C;Date: 02-JUL-1996
C:Accession: I48744

C;Accession: 148/44
P. Buschschol A W : Adams P H : Betz H

R;Puschel, A.W.; Adams,
Newborn 14 041-049 1995

Neuron 14, 941-948, 1995

A:Reference number: I48744; MUID:95267431; PMID:7748561

A:Accession: I48744

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-748 <RES>

A:Cross-references: UNIPROT:Q62177; EMBL:X85990; NID:g854323; PIDN:CAAS9982.1; PID:g8543

C:Genetics:

A:Gene: sema

C:Superfamily: semaphorin

Alignment Scores:

Pred. No.: 1.32e-147 Length: 748
Score: 2059.50 Matches: 400
Percent Similarity: 66.93% Conservative: 112
Best Local Similarity: 52.23% Mismatches: 184
Query Match: 42.06% Indels: 69
DB: 2 Gaps: 15

US-09-774-490-1 (1-2709) x I48744 (1-748)

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QY 281 RATGTGCCAAGCTGAATATCTTACAAAGAAATGTTGGAATCCAAACAATGTGATCACT 340
Db 27 AenLeuProArgLeuArgLeuSerPheGlnGluLeuGlnAlaArgHisGlyValArgThr 46
QY 341 TTCAATGGCTTGGCCAAAGCTCCAGTTCATACCTCTTTCGATGAGGAAACGGAGT 400
Db 47 PheArg--LeuGluArgThrCysCysTyrGluAlaLeuLeuValAspGluArgGly 65
QY 401 AGCGTGTATGTGGAGAAAGATCACATATTTTCATTCGACCTGGTAAATATC---AAG 457
Db 66 ArgLeuPheValGlyAlaGluAsnHisValAlaSerLeuSerLeuAspAsnIleSerLys 85
QY 458 GATTTTCAAAAGATTGTGGCCAGTACTTACACAGAGAGATGAATGCAAGTGGCT 517
Db 86 ArgAlaLysLeuLeuAlaTyrProAlaProValGluTyrArgGluGluCysAsnTrpAla 105
QY 518 GGAAGAGACATCCTCAAGAAATGCTAATTTTCATCAAGGTACTTAAAGCATATAATCAG 577
Db 106 GlyLysAspIleGlyThrGluCysMetAsnPheValArgLeuLeuHisAlaTyrAsnHis 125
QY 578 ACTCTACTGTAGCGTGTGGAAAGCGGGCTTTTCATCCAAATTCG----- 622
Db 126 ThrHisLeuLeuAlaCysArgThrGlyAlaPheHisProThrCysAlaLeuTrpArgTrp 145
QY 623 -----ACCTACATTGAAATGGACATCATCTCGAGGACAAATATTTTAAG 667
Db 146 AlaThrAlaGlyThrHisAlaSerThrGly-----ProGlu----- 158
QY 668 CTGGAGAACTCACATTTTGAACCGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTG 727
Db 159 -----LysLeuGluAspGlyLysGlyLysThrProTyrAspProArgHisArg 174
QY 728 ACAGCATCCCTTTTAATAGATGGAATATATCTCTGGAACCTGACGTGATTTATGGGG 787
Db 175 ProProSerValLeuValGlyGluLeuTyrSerGlyValThrAlaAspLeuMetGly 194
QY 788 CGAGACTTGTCTCTCGAACTCTGGCCACCACCCCAATCAGGACGACGAGCAT 847
Db 195 ArgAspPheThrIlePheArgSerLeuGlyGlnAsnProSerLeuArgThrGluProHis 214
QY 848 GATTCAGGTGGCTCAATGATCCAAAGTTCAATTAGTGGCCACCTCATCTCAGAGAGTGCAC 907
Db 215 AspSerArgTrpLeuAsnGluProLysPheValLysValPheTrpIleProGluSerGlu 234
QY 908 AATCTGAAGATGACAAAGTATATCTTTCTTCCTGAAATGCAATAGATGGGAACAC 967
Db 235 AsnProAspAspLysIleTyrPhePheArgGluSerAlaValGluAlaAlaPro 254
QY 968 TCT---GGAAGAGTACTCACCTAGATAGTTCAGATATGCAAGATGCTTTTGAGGG 1024
Db 255 AlaMetGlyArgMetSerValSerArgValGlyGlnIleCysArgAsnAspLeuGly 274
QY 1025 CACGAAGTCTGGTGAATAAATGGACAAATTCCTCAAAAGCTCGTCTGATTTGCTCAGTG 1084

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Db 275 GlnArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerVal 294
QY 1085 CCAGTCCAAATGGCATTCAGACTCATTTTATGATGACAGTGCAGGATGTATTCCTAATGAAC 1144
Db 295 ProGlyValGluGly--AspThrHisPheAspGlnLeuGlnAspValPheLeuLeuSer 313
QY 1145 TTTAAGATCCTAAAAATCCAGTTGTATATGGAGTGTGTACGACTTCAGTAACATTTTC 1204
Db 314 SerArgAspArgGlnThrProLeuLeuTyrAlaValPheSerThrSerSerGlyValPhe 333
QY 1205 AAGGATCAGCCGCTGTGTATGTATAGCATGTGTGAGAGAGGCTGTTCCTTGGTCCA 1264
Db 334 GlnGlySerAlaValCysValTyrSerMetAsnAspValArgArgAlaPheLeuGlyPro 353
QY 1265 TATGCCACACAGGATGGACCCCACTATCAATGGGGCTTATCAAGGAGAGTCCCTTAT 1324
Db 354 LeuProHisLysGluGlyProThrHisGlnTrpValSerTyrGlnGlyArgValProTyr 373
QY 1325 CCAGGCCAGAACCTGTGCCAGAAAACATTTGGTGGTGTGTGACTCTACAAAGGACCTT 1384
Db 374 ProArgProGlyMetCysProSerLysThrPheGlyThrPheSerSerThrLysAspPhe 393
QY 1385 CCTGATGATGTTAAACCTTTTCAAGAAAGTCCATCCAGCCATGTACAATCCAGTGTTCCT 1444
Db 394 ProAspAspValIleGlnPheGlyArgAsnHisProLeuMetTyrAsnProValLeuPro 413
QY 1445 ATGAACAATCCCCCAATAGTATCAAAACGAGTGAATTAATCAATTTTACACAAATGTC 1504
Db 414 MetGlyArgProLeuPheLeuGlnValGlyAlaGlyTyrThrPheThrGlnIleAla 433
QY 1505 GTAGACCCAGTGGATGACAGAGATGGACAGATGATGATGTTTATCGGAACACATGTT 1564
Db 434 AlaAspArgValAlaAlaAspGlyHisTyrAspValLeuPheIleGlyThrAspVal 453
QY 1565 GGGACCGTCTTAAAGTAGTTTCAATTCCTAAGGAGACTGTGTATGATTTTAAAGAGGTT 1624
Db 454 GlyThrValLeuLysValIleSerValProLysGlyArgArgProAsnSerGluGlyLeu 473
QY 1625 CTGCTGGAAGAAATGACAGATTTTTCGGGAACCGAGTCTATTTTACGCAATGGAGCTTCC 1684
Db 474 LeuLeuGluGluLeuGlnValPheGluAspSerAlaAlaIleThrSerMetGlnIleSer 493
QY 1685 ACTAAGACGACCAACTATATATTGTTCAACCGCTGGGCTTGCACACTCCCTTTTACAC 1744
Db 494 SerLysArgGlnGlnLeuTyrValAlaSerArgAlaAlaValAlaGlnIleAlaLeuHis 513
QY 1745 CGTGTGTATATTTACGGGAAACGCTGCTGAGTGTTCCTCGCTCGCCGAGACCTTACTGT 1804
Db 514 ArgCysThrAlaLeuGlyArgAlaCysAlaGluCysCysLeuAlaArgAspProTyrCys 533
QY 1805 GCTTGGGATGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCACAGAGA 1864
Db 534 AlaTrpAspGlySerAlaCysThrArgPheGlnProThrAlaLysArgArgPheArg 553
QY 1865 CAAGATATAAGAAATGGAGACCACTGACTCACTGTTTTCAGACTTACACCATGATATAC 1924
Db 554 GlnAspIleArgAsnGlyAspProSerThrLeuCysSerGly-----AspSerSer 570
QY 1925 CATGCCACACCCCTGAAGAGAGAGATCATCATGTGTGTAGAGAAATAGTAGCACTTTTG 1984
Db 571 HisSerValLeuLeuGluLysValLeu---GlyValGluSerGlySerAlaPheLeu 589
QY 1985 GAATGCATCGAAGTCCAGAGAGCGCTGCTTATTCGCAATTCAGGCGGGAATGAA 2044
Db 590 GluCysGluProArgSerLeuGlnAlaHisValGlnTrpThrPheGlnGlyAlaGlyGlu 609
QY 2045 GAGCGAAAGAGAGATCAGAGTGGATCATATCATCATCATCAGACAGATCAAGCGCTTCTG 2104
Db 610 AlaAlaHisThrGlnValLeuAlaGluGluArgValGluArgThrAlaArgGlyLeuLeu 629
QY 2105 CTACGTAGTCTACAAACAGAGAGATTACCGCAATTTACCTCTCGCATCGCGGTGGAACATGGG 2164

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Db 445 ArgTyrGluValLeuPheLeuGlyThrAspArgGlyThrValGlnLysValleValLeu 464
 QY 1592 CTAAGGAGACTTGGTATGATTAGAGAGGTTCTGCTGGAAGAATGACAGTCTTTTCGG 1651
 Db 465 ProLysAspAsp---GlnGluMetGluLeuMetLeuGluGluValGluValPheLys 483
 QY 1652 GAACGAGCTGTTATTCAGCAATGGAGCTTCCATTAAGCAGCAACAATATATATATGTT 1711
 Db 484 AspProAlaProValLysThrMetThrLysSerLysArgGlnGlnLeuTyrValAla 503
 QY 1712 TCACGGCTGGGTGCCAGCTCCCTTTACACCGGTGTGATATTACGGGAACGGTGT 1771
 Db 504 SerAlaValGlyValThrHisLeuSerLeuHisArgCysGlnAlaTyrGlyAlaCys 523
 QY 1772 GCTGAGTGTGCTCGCCGAGACCTTACTGCTGCTGGATGGTTCGATGTTCTGCG 1831
 Db 524 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTTPaspGlyGlnAlaCysSerArg 543
 QY 1832 TATTTTCCCACTGCCAAGAGACGCAAGACGACAGATATTAAGAAATGGAGACCCACTG 1891
 Db 544 TyrThrAlaSerSerLysArgArgSerArgArgGlnAspValArgHisGlyAsnProLe 563
 QY 1892 ACTCACTGTTACAGCTTACACATGATATACCATGATGCGCCAGCCCTGACAGAGATC 1951
 Db 564 ArgGlnCysArgGlyPhe-----AsnSerAsnAlaAsnLysAsnAlaValGluSerVal 581
 QY 1952 ATCTATGTTAGAGAAATAGTACACATTTTGGATGAGTCCGAGTCCGAGAGAGCG 2011
 Db 582 GlnTyrGlyValAlaGlySerAlaAlaPheLeuGluCysGlnProArgSerProGlnAla 601
 QY 2012 CTGCTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAAGAGAGATGAGTGGAT 2071
 Db 602 ThrValLysTrpLeuPheGlnArgAspProGlyAspArgArgGluLeuAlaGlu 621
 QY 2072 GATCATATCATCAGACAGATCAAGCCCTTCTGCTAGCTAGTCTACACAGAGATTC 2131
 Db 622 AspArgPheLeuArgThrGluGlnGlyLeuLeuLeuArgAlaLeuGlnLeuSerAspArg 641
 QY 2132 GCAATTAACCTCGCCATCGGTGGAAACATGGGTTTCATACAACTCTTCTTAAGGTAA 2191
 Db 642 GlyLeuTyrSerCysThrAlaThrGluAsnAsnPheLysHisValValThrArgValGln 661
 QY 2192 CTGGAAGTCATTCACACAGCATTTTGAAGAACTTCTTCAATAAGATGATGATGAGAT 2251
 Db 662 LeuHisValLeuGlyArgAspAlaValHisAlaAlaLeuPhe----- 675
 QY 2252 GCTCTAAGACCAAGAAATGCTCAATAGCATGACACCTAGCCAGAGAGTCTGG----- 2305
 Db 676 -----ProProLeuSerMetSerAlaProProProProGlyAlaGlyProPro 691
 QY 2306 -----TACAGAGCTTCATGAGCTCATCAACCCCACTCAACACGATGGAT 2356
 Db 692 ThrProProTyrGlnGluLeuAlaGlnLeuLeuAlaGlnProGluValGlyLeuLeuHis 711
 QY 2357 GAGTCTCTGGAACAATTGGAAGAGGACCGAAACAAACAGTCTGGCAAGGCCAGACAT 2416
 Db 712 GlnTyrCysGlnGlyTyrTrpArgHisValProProSerProArgGluAlaProGly--- 730
 QY 2417 ACCCAGGGAACAGTACAAATGGAAGACCTTACAGAAATAAGAAAGGTAGAACAGG 2476
 Db 731 -----AlaProArgSerProGluProGlnAspGlnLysLysProArgAsnArg 746
 QY 2477 AGGACCCAC 2485
 Db 747 ArgHisHis 749

RESULT 8
 I48748
 semaphorin E - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I48748
 R:Puschel, A.W.; Adams, R.H.; Betz, H.

Neuron 14, 941-948, 1995
 A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
 A:Reference number: I48744; MUID:95267431; PMID:7748561
 A:Accession: I48748
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-751 <RES>
 A:Cross-references: UNIPROT:Q62181; EMBL:X85994; NID:g854331; PIDN:CAAS9986.1; PID:g85433
 C:Gene: semE
 C:Superfamily: semaphorin

Alignment Scores:
 Pred. No.: 8,47e-132 Length: 751
 Score: 1850.50 Matches: 343
 Percent Similarity: 65.54% Conservative: 161
 Best Local Similarity: 44.60% Mismatches: 224
 Query Match: 37.80% Indels: 41
 DB: 2 Gaps: 10

US-09-774-490-1 (1-2709) x I48748 (1-751)

QY 215 AGGATGTTCTGCTCTTTCTGGGAGTATTACTTACAGCAAGAGCAAACTATCAGATGGG 274
 Db 4 ArgAlaIleCysValLeuValGlyValPheIleCysSerIleCys---ValArgGlySer 22
 QY 275 AAGAACAAATGTGCCAAGGCTGAAATATCTCTACAAAGAAATGTTGGAATCCAAACAATGTG 334
 Db 23 SerGlnProGlnAlaArgValTyrLeuThrPheAspGluLeuArgGluThrLysThrSer 42
 QY 335 ATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCATACCTCTCTTTGGATGAGAA 394
 Db 43 GluTyrPheSerLeuSerHisGlnGlnLeuAspTyrArgIleLeuLeuMetAspGluAsp 62
 QY 395 CGGAGTAGCTGTATGTTGGAGCAAGCATCACATATTTTCTTATTCGACTCGTTAATATC 454
 Db 63 GlnAspArgIleTyrValGlySerLysAspHisIleLeuSerLeuAsnIleAsnIle 82
 QY 455 ---AAGAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAATGCAAG 511
 Db 83 SerGlnGluProLeuSerValPheTrpProAlaSerThrIleLysValGluGluCysLys 102
 QY 512 TGGGCTGGAAGAAGACATCCTGAAAGATGTGCTTAATTTTCATCAAGGTACTTAAAGCATAT 571
 Db 103 MetAlaGlyLysAspProThrHisGlyCysGlyAsnPheValArgValIleGlnThrPhe 122
 QY 572 AATCAGACTCACTGTAGCCCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATT 631
 Db 123 AsnArgThrHisLeuTyrValCysGlySerGlyAlaPheSerProValCysThrTyrLeu 142
 QY 632 GAAATTTGGACATCATCTCTGAGGACAAATATTTTAACTGGAGAACTCACATTTTCCGAAC 691
 Db 143 AsnArgGlyArgArgSerGluAspGlnValPheMetIleAsp---SerLysCysGluSer 161
 QY 692 GGCCGTGGGAAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTTTTAAATAGATGA 751
 Db 162 GlyLysGlyArgCysSerPheAsnProAsnValAsnThrValSerValMetIleAsnGlu 181
 QY 752 GAATTTACTCTGGAACTGCACCTGATTTTATGGGCGGAGCTTTGCTATCTTCCGAAC 811
 Db 182 GluLeuSerGlyMetTyrIleAspPheMetGlyThrAspAlaAlaIlePheArgSer 201
 QY 812 CTTGGGCGCCACCACCCCAATCAGGACAGCAGCATGATTCAGGTGGCTCAATGATCCA 871
 Db 202 LeuThrLysArgMetGlnLeuArgThrAspGlnHisAsnSerLysTrpLeuSerGluPro 221
 QY 872 AAGTTCAATAGTCCACCTCATCTCAGAGAGTGAATCCCTGAAGATGACAAAGATATAC 931
 Db 222 MetPheValAspAlaHisValIleProAspGlyThrAspProAsnAspAlaLysValTyr 241
 QY 932 TTTTCTTCTCCGTGAAATGCAATAGATGAGAACACTCTCGGAAAGCTTACTCAGCTAGA 991
 Db 242 PhePhePheLysGluArgLeuThrAspAsnAsnArgSerThrLysGlnIleHisSerMet 261

QY 992 ATAGTCAGATATGCAAGAAATGACTTTTGGAGGCGCAGCAAGTCTGGTGAATAAATGGACA 1051
DB : : : : :
DB 262 IleAlaArgIleCysProAsnAspThrGlyGlnArgSerLeuValAsnIleYsrPrThr 281
QY 1052 ACATTCTCAAAGCTCGTCTGATTGCTCAGTGCAGGCTCCAAATGGCAATTCACACTCAT 1111
DB : : : : :
DB 282 ThrPheLeuLeuYalaArgLeuValCysSerValThrAspGluAspGlyProGluThrHis 301
QY 1112 TTGTGTAAGTCCAGGATGATTCTTAATGAATCTTAAAGATCTTAAATAATCCAGTTGTA 1171
DB : : : : :
DB 302 PheAspGluLeuGluAspValPheLeuLeuGluThrAspAsnProArgThrThrLeuVal 321
QY 1172 TATGAGTGTTCAGATCTCCAGTAACATTTCAAGGATCAGCGTGTGTATGTATAGC 1231
DB : : : : :
DB 322 TyrGlyIlePheThrThrSerSerValPheLeuGlySerAlaValCysValTyrHis 341
QY 1232 ATGAGTGTGTGAGAAGGTGTTCTTGTCTCATATGCCACAGGATGGACCAACTAT 1291
DB : : : : :
DB 342 LeuSerAspIleGlnThrValPheAsnGlyProPheAlaHisGlyGluGlyProAsnHis 361
QY 1292 CAATGGTGCCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGAACCTTGTCCAGCAA 1351
DB : : : : :
DB 362 GlnLeuIleSerTyrGlnGlyArgIleProTyrProArgProGlyThrCysProGlyGly 381
QY 1352 ACATTT---GGTGGTTTGACTCTACAAAGACCTTCTGTATGATGTATTAACCTTTGCA 1408
DB : : : : :
DB 382 AlaPheThrProAsnMetArgThrThrLysAspPheProAspValValThrPheIle 401
QY 1409 AGAAGTCATCCAGCATGATACATCCAGTGTTCCTATCAACAATCGCCCAATAGTATC 1468
DB : : : : :
DB 402 ArgAsnHisProLeuMetTyrAsnSerIleSerProIleHisArgArgProLeuIleVal 421
QY 1469 AAAACGGATGTAATATCAATTTACAAATTTGCTAGACCGAGTGGATGACAGAGAT 1528
DB : : : : :
DB 422 ArgIleGlyThrAspTyrLysThrLysIleAlaValAspArgValAsnAlaAlaAsp 441
QY 1529 GGACAGTATGATGTATGTTATCGGAACAGATGTGGACCGTCTTAAAGTAGTTTCA 1588
DB : : : : :
DB 442 GlyArgTyrHisValLeuPheLeuGlyThrAspArgGlyThrValGlnLysValValVal 461
QY 1589 ATTCCTAAGGACACTGGTATGATTTAGAAAGGTCTCTCGAAGAATGACAGTTT 1648
DB : : : : :
DB 462 LeuProThrAsnSerSerAlaSer---GlyGluLeuLeuGluLeuGluValPhe 480
QY 1649 CCGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACACTATAT 1708
DB : : : : :
DB 481 LysAsnHisValProIleThrThrMetGluIleSerSerLysLysGlnGlnLeuTyrVal 500
QY 1709 GGTTCACCGCTGGGTGCCAGTCCCTTTACACCGGTGTGATATTTACGGGAAGCG 1768
DB : : : : :
DB 501 SerSerAsnGluGlyValSerGlnValSerLeuHisArgCysHisIleTyrGlyThrAla 520
QY 1769 TGTGCTGAGTGTGCTCCCGCAGACCCCTTACTGTGTTGGATGGTTCATGTTCT 1828
DB : : : : :
DB 521 CysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTyrAspGlyHisSerCysSer 540
QY 1829 CGCTATTTCCCAAGAGAGCGCACAGACAGATATTAAGAAATCGAGACCCA 1888
DB : : : : :
DB 541 ArgPheTyrProThrGlyLysArgSerArgGlnAspValArgHisGlyAsnPro 560
QY 1889 CTGACTCTACTGTTACAGCTTACACCATGATATACCATGGCCAGCCCTCGAAGAGA 1948
DB : : : : :
DB 561 LeuThrGlnCysArgGlyPheAsnLeuLysAlaTyr-----ArgAsnAlaAlaGluIle 578
QY 1949 ATCATCTATGTTGATAGAAATAGTACACATTTTGGAAATGAGTCCGGAAGTCGAGAGA 2008
DB : : : : :
DB 579 ValGlnTyrGlyValArgAsnAsnSerThrPheLeuGluCysAlaProLysSerProGln 598
QY 2009 GCGCTGCTATTTGCAATTCAGAGCGCAATTAAGACGCGAAAGAGATCAGATG 2068
DB : : : : :
DB 599 AlaSerIleLysTyrLeuLeuGln---LysAspLysAspArgLysGluGlyLysLeu 617

QY 2069 GATGATCATATCATCAGGACATCAAGGCTTCTGCTAGCTACTACACAGAGGAT 2128
DB : : : : :
DB 618 AsnGluArgIleAlaThrSerGlnGlyLeuLeuIleArgSerValGlnAspSerAsp 637
QY 2129 TCAGGCAATTTACTCTGCGCATGCGGTGGAACATGGGTTTCATACAACTCTTCTTAAGTA 2188
DB : : : : :
DB 638 GlnGlyLeuTyrHisCysIleAlaThrGluAsnSerPheLysGlnThrIleAlaLysIle 657
QY 2189 ACCCTGGAAGTCAATTGACACAGAGCATTTGGAAGAACTTCTTCATAAAGATGATGGA 2248
DB : : : : :
DB 658 AsnPheLysValLeuAspSer----- 664
QY 2249 GATGCTCTAAGACCAAGAAATGTCCTAATAGCATGACACCTAGCCAGAGGCTCTGGTAC 2308
DB : : : : :
DB 665 -----GluMetValAlaValThrAspLysTyrSerProTyrThr 678
QY 2309 -----AGAGACTTCATGCGCTCATCAAC 2332
DB : : : : :
DB 679 TrpAlaGlySerValArgAlaLeuProPheHisProLysAspIleLeuGlyAlaPheSer 698
QY 2333 CACCCCAATCTCAACACGATGATGTTCTGTGAACAGTGTGGAAAGAGGACCGCAAAA 2392
DB : : : : :
DB 699 HisSerGluMetGlnLeuIleAsnGlnTyrCysLysAspThr-----ArgGlnGlnGln 716
QY 2393 CACCTCGCGCAAGCCAGGACATACCCAGGGAACAGTAACAATGGAAGCACTTACAA 2452
DB : : : : :
DB 717 GlnLeuGlyGluGluProGlnLysMetArgGlyAspTyrGlyLysLeuLysAlaLeuIle 736
QY 2453 GAAATAAGAAAGGTAGAAACAGGAGG 2479
DB : : : : :
DB 737 AsnSerArgLysSerArgAsnArgArg 745

RESULT 9
S66498
M-sema F protein precursor - mouse
C.Species: Mus musculus (house mouse)
C.Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C.Accession: S66498
R.Inagaki, S.; Furuyama, T.; Iwahashi, Y.
FEBS Lett. 370, 269-272, 1995
A.Title: Identification of a member of mouse semaphorin family.
A.Reference number: S66498; MUID:95385809; PMID:7656991
A.Accession: S66498
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-834 <INA>
A.Cross-references: UNIPROT:Q64151; EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110598
C.Superfamily: semaphorin
F1-21/Domain: signal sequence #status predicted <SIG>
F1-22-834/Product: M-sema F protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 6, 88e-65 Length: 834
Score: 966.00 Matches: 236
Percent Similarity: 51.3% Conservative: 107
Best local Similarity: 35.3% Mismatches: 269
Query Match: 19.7% Indels: 56
DB: 2 Gaps: 21

US-09-774-490-1 (1-2709) x S66498 (1-834)

QY 206 TGGTTAACTAGGATGTCTGCTTTTCTGGGAGTATTACTTACAGCAAGACAAACTAT 265
DB : : : : :
DB 8 TrpLeu-----LeuAlaAlaGlyLeuTyrGlyLeuGlyIleGlyAlaGluMetTyrTrp 25
QY 266 CAGAATGGGAAGAACAAATGTGCCAAGCGTGAATATCTCTCAAAAGAAATGTTGGAATCC 325
DB : : : : :
DB 26 -----AsnLeuValProArgLysThrValSerSerGlyGluLeuValThrVal 41
QY 326 AACATGTGATCATCTTCAATGGCTTGGCCACAGCTCCAGTTATCATCATCTCTTTT 385
DB : : : : :
DB 42 ValArgArgPheSerGlnThrGlyIle-----GlnAspPheLeuThrLeuThrLeu 58

Qy	386	GATCAGAAACGGAGTAGCTGTATGTTGGAGCAAGGATCACATATATTTTCATTCCAGCTG	445
Db	59	ThrGluHisSerGlyLeuLeuTyrValGlyAlaArgGluAlaPheAlaPheSerVal	78
Qy	446	GTTAATATCAAGGATTTTCAAAGATGTGTGGCCAGTCATCTTACACCAAGAGATGAA	505
Db	79	GluAlaLeuGluLeuGlnGlyAlaIleSerTyrGluAlaProAlaGluIlySlyIleGlu	98
Qy	506	TGCAAGTGGGTGGAAAGACATCCTGAAAGAATGTCTAATTTTCATCAAGGTACTTAAG	565
Db	99	CysThrGlnIlySGLyLysSerAsnGlnThrGluCysPheAsnPheIleArgPheLeuGln	118
Qy	566	GCATATTAATCAGACTCATCTGTAGCCTGTGGAAACGGGGGCTTTTCATCCAAATTTGCACC	625
Db	119	ProTyrAsnSerHisLeuTyrValCysGlyThrTyrAlaPheGlnProLysCysThr	138
Qy	626	TACATTGAAATGGACATCATCCTCGAGGACAAATATTTTAAGCTGGGAGAACTCACATTTT	685
Db	139	TyrIleAsnMet-----LeuThrPheThrLeuAspArgAlaGluPhe	152
Qy	686	GAAACGGCCCTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTTTTAATA	745
Db	153	GluAspGlyLysGlyLysCysProTyrAspProAlaIlySGLyHisThrGlyLeuLeuVal	172
Qy	746	GATGGAGAATPATACTCTGGAACCTGCAGCTCAATTTATGGGGCGAGACTTTGCTATCTTC	805
Db	173	AspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeuGlyThrGluProValIleLeu	192
Qy	806	CGAACTCTTGGGCACCAACCCCAATCAGGACAGCAGCATGATTCACAGTGGCTCAAT	865
Db	193	ArgTyrMetGlyThrHisHisSerIleLysThrGlu--TyrLeuAlaPheTyrLeuAsn	211
Qy	866	GATCAAAAGTTCAATTAGTGGCCCACTCATCTCACAGAGTCACAATCCT-----GAA	916
Db	212	GluProHisPheValGlySerAlaPheValProGluSerValGlySerPheThrGlyAsp	231
Qy	917	GATGACAAAGPATACTTTTCTCCGTGAAAAATGCAATAGATGAGAGAACTCTGGAAAA	976
Db	232	AspAspIlyIleTyrPhePhePheSerGluArgAlaValGluTyrAspCysTyrSerGlu	251
Qy	977	GCTACTCACGCTAGAATAGTGCATATGCAAGAAATGACTTTGGAGGGCACAGAGTCTG	1036
Db	252	GlnValValAlaArgValAlaArgValCysIlySGLyAspMetGlyGlyAlaArgThrLeu	271
Qy	1037	GTGAATAATCGACAAACATCTCCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCACAAAT	1096
Db	272	GlnIlySlyIleTyrThrPheLeuIlyAlaArgLeuValCysSerAlaPro-----	288
Qy	1097	GGCATTGACACTCATTTTGATGAATCGCAGGATGATTTCCCTAATGAATCTTAAAGATCCT	1156
Db	289	AspTyrIlySValTyrPheAsnGlnLeuIlySAlaValHisThrLeuArgGlyAlaSerTyr	308
Qy	1157	AAAAATCCAGTTGATATGAGTGTTTACGACTTCCAGTCAACATTTTCAAGGATACGCC	1216
Db	309	HisAsnThrThrPhePheGlyValPheGlnAlaArgTyrGlyAspMetAspLeuSerAla	328
Qy	1217	GTGTGTATGTATAGCATCAGTGTGTGAGAAGGGTGTCTTGTGTCCATATGCCACAGG	1276
Db	329	ValCysGluTyrGlnLeuGluGlnIleGlnValPheGluGlyProTyrIlySGLuTyr	348
Qy	1277	GATGGACCAACTATCAATGGGTGCCCTTATCAAGGAAGAGTCCCTATCCACGGCCAGGA	1336
Db	349	SerGluGlnAlaGlnIlyTyrAlaArgTyrThrAspProValProSerProArgProGly	368
Qy	1337	ACTGTGCCAGAAACAAATTT-----GGTGGTTTTGACTCTCAAAAGGACCTTCTGAT	1390
Db	369	SerCysIleAsnAsnTyrHisArgAspAsnGlyTyrThrSerSerLeuGluLeuProAsp	388
Qy	1391	GATGTTATAACCTTTGCAAGAAGTCATCCACCACTGTACAATCCAGTGTTCCTATGAAC	1450
Db	389	AsnThrLeuAsnPheIleLysLysHisProLeuMetGluAspGlnValIlySProArgLeu	408
Qy	1451	AATCGCCCAATAGTCATCAAAACGGATGTAATTTATCAATTTTACACAAATTTGCTAGAC	1510

Db	409	GlyArgProLeuLeuValLysLysAsnThrAsn-----PheThrHisValValAlaAsp	426
QY	1511	CGAGTGTGATGCAGAAAGATGGA--CAGTATGATGTTATGTTATTCGGAACAGATGTTGGG	1567
Db	427	ArgValProGlyLeuAspGlyAlaThrTyrThrValLeuPheIleGlyThrGlyAspGly	446
QY	1568	ACCGTTCTTAAAGTAGTTTCAATCTCCAAAGAGACTTGGTATGATTAGTAAGAGGTTCTG	1627
Db	447	TrpLeuLeuLysAlaValSerLeu-----GlyProTrpIleHis-----Met	460
QY	1628	CTGCAAGAAATGACAGTTT---CGGGAACCGACTGCTTATTTACGAATGGAGCTTTCC	1684
Db	461	ValGluGluLeuGlnValPheAspGlnGluPro-----ValGluSerLeuValLeuSer	478
QY	1685	ACTAAGCAGCAACAACTATATATTGGTTCAACGGCTGGGTTCCCGAGTCTCCCTTTACAC	1744
Db	479	GlnSerLysLysValLeuPheAlaGlySerArgSerGlnLeuValGlnLeuSerLeuAla	498
QY	1745	CGGTGTGATATTATTCGGGAAAGCGTGTGCTGAGTGTTCCTCCCGCAGACCTTACTGT	1804
Db	499	AspCysThrLysTyr---ArgPheCysValAspCysValLeuAlaArgAspProTyrCys	517
QY	1805	GCTTGGGATGGTCTCGCATGTTCTCGCTATTTTCCCACTCTCAAGAGAGACCAACAGCGA	1864
Db	518	AlaTrpAsnValAsnThr---SerArgCysValAlaThrThrSerGlyArgSerGlySer	536
QY	1865	-----CAAGATATAAGAAATGGAGACCCACTGACTCACCTGTTTCAGACTTACACCAT	1915
Db	537	PheLeuValGlnHisValAlaAsnLeuAspThrSerLysMetCys-----	551
QY	1916	GATAATCACCATGGCCACAGCCCTCGAAGAGAGAATC-----ATCTATGTGTGAGAG	1966
Db	552	--AsnGlnTyrGlyIleLysLysValArgSerIleProLysAsnIleThrValValSer	570
QY	1967	AATAGTAGCACATTTTGGAAATGCGATCCGCAAGTCCGAGACAGCGCTGCTATTGGCAA	2026
Db	571	GlyThrAspLeuValLeuProCysHisLeuSerSerAsnLeuAlaHisAlaHisTrpThr	590
QY	2027	TTC-----CAGAGCGCAATGAAGCGCAAAAGAGAGATCAGAGTGGATGATCATATC	2080
Db	591	PheGlySerGlnAspLeuProAlaGluGlnProGlySerPheLeuTyrAspThrGlyLeu	610
QY	2081	ATCAGGACAGATCAAGCCCTTCTGCTACGTAGTCTACAAACAGAAAGGATTTCAGCAATTAC	2140
Db	611	-----GlnAlaLeuValValMetAlaAlaGlnSerArgHisSerGlyProTyr	626
QY	2141	CTCTGCCATCGGTGGAACTGGG	2164
Db	627	ArgCysTyrSerGluGlnGlnGly	634
RESULT 10			
semaphorin C - mouse (fragment)			
C:Species: Mus musculus (house mouse)			
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I48746			
R:Puschel, A.W.; Adams, R.H.; Betz, H.			
Neuron 14, 941-948, 1995			
A>Title: Murine semaphorin D/collapsin is a member of a diverse gene family and			
A:Reference number: I48744; MUID:95267431; PMID:7748561			
A:Accession: I48746			
A>Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-782 <RSS>			
A:Cross-references: UNIPROT.Q62179; EMBL.X85992; NID:g854327; PIDN:CAA59984.1;			
C:Genetics:			
A:Gene: semC			
C:Superfamily: semaphorin			
Alignment Scores:			
Pred. No.:		1.1e-56	Length:
Score:		857.50	Matches:
			217

Percent Similarity: 49.77% Conservative: 114
 Best Local Similarity: 32.63% Mismatches: 261
 Query Match: 17.51% Indels: 73
 DB: 2 Gaps: 23

US-09-774-490-1 (1-2709) x 148746 (1-782)

QY 356 AACAGCTCCAGTATCATACCTTCCTTTGGATGAGAACGGAGTAGGCTGTATGTGA 415
 DB 12 AsnIleSerAsnTrpThrAlaLeuLeuLeuSerGlnAspGlyLysThrLeuTrpValGly 31
 QY 416 GCAAGAGTACACATATTTTCATTCGACCTGGTGTAAATCAAG-----GAT 460
 DB 32 AlaArgGluAlaLeuPheAlaLeuAsn---SerAsnLeuSerPheLeuProGlyGlyGlu 50
 QY 461 TTTCAAAGATTGTGGCCAGTATCTTACACAGAGAGAGATGAATCGAAGTGGCTGGA 520
 DB 51 TyrGlnGluLeuLeuTrpSerAlaAspAlaAspArgLysGlnGlnCysSerPheLysGly 70
 QY 521 AAGACATCTGAAAGATGTGCTAATTCATCAAGTACTTAAGCATATATACACT 580
 DB 71 LysAspProLysArgAspCysGlnAsnTrpIleLysIleLeuLeuProLeuAsnSerSer 90
 QY 581 CACTCTGACGCTGCGAAGGGGGCTTTTCATCCCAATTGCACTACACTGAATTTGA 640
 DB 91 HisLeuLeuThrCysGlyThrAlaAlaPheSerProLeuCysAlaTrpIleHisIleAla 110
 QY 641 CATCATCTCGAGACAATATTTTAAAGCTGGAG-----AACTCACATTTT 685
 DB 111 Ser-----PheThrLeuAlaGlnAspGluAlaGlyAsnValIleLeu 124
 QY 686 GAAACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGATCCCTTTTAATA 745
 DB 125 GluAspGlyLysGlyHisCysProPheAspProAsnPheLysSerThrAlaLeuVal 144
 QY 746 GATGGAATATACCTGGAAGTGGAGTATTTTATGGGGCAGACTTGTCTATCTTC 805
 DB 145 AspGlyGluLeuTrpThrGlyThrValSerSerPheGlnGlyAsnAspProAlaIleSer 164
 QY 806 CGAATCTTGGGCACCAACCAATCAGGACAGAGCAGCATGATCCAGGTGGCTCAAT 865
 DB 165 ArgSerGlnSer---SerArgProThrLysThrGluSer---SerLeuAsnTrpLeuGln 182
 QY 866 GATCCAAAGTTCATTAGTCCCACTCATCTCAGACAGT---GACAATCCT-----GAA 916
 DB 183 AspProAlaPheValAlaSerAlaThrSerProGluSerLeuGlySerProIleGlyAsp 202
 QY 917 GATGACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGAAA 976
 DB 203 AspAspLysIleTrpPhePheSerGluThrGlyGlnGluPheGluPheGluAsn 222
 QY 977 GCTACTCAGCTAGATAGTGCAGATATGCAAGATGACTTTGGAGGCGACAGAGCTG 1036
 DB 223 ThrIleValSerArgValAlaArgValCysLysGlyAspGluGlyGluArgValLeu 242
 QY 1037 GTGAATAAATGGACAACATCTCTCAAGCTCGCTGATTTGCTCAGTGGCAGTCCAAAT 1096
 DB 243 GlnGlnArgTrpThrPheLeuLysAlaGlnLeuLysCysSerArgPro---AspAsp 261
 QY 1097 GGCATTGACACTCATTTGATGAACTGCGAGATGATTTCTTAATG-----AACTTTAA 1150
 DB 262 GlyPhePro-----PheAsnValLeuGlnAspValPheThrLeuAsnProAsnProGln 279
 QY 1151 GATCCTTAAATCCAGTGTATATGAGTGTATTACCATCTCC-----AGTAACTTTTC 1204
 DB 280 AspTrpArgLysThrLeuSerIleGlyValPheThrSerGlnTrpHisArgGlyThrThr 299
 QY 1205 AAGGGATCAGCGTGTGTATAGCATGAGTGTGAGAGGGTGTCTTCTGTGCTCA 1264
 DB 300 GluGlySerAlaIleCysValPheThrMetAsnAspValGlnLysAlaPheAspGlyLeu 319
 QY 1265 TATGCCCAAGGATGGACCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTAT 1324

DB 320 TyrLysLysValAsnArgGluThrGlnGlnTrpTyrThrGluThrHisGlnValProThr 339
 QY 1325 CCACGCCAGGAACCTGT-----CCACGAAACAACTTTGGTGGTCTACTACAAG 1378
 DB 340 ProArgProGlyAlaCysIleThrAsnSerAlaArgGluArgLysIleAsnSerSerLeu 359
 QY 1379 GACCTTCCTGATGATGTTATACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTG 1438
 DB 360 GlnLeuProAspArgValLeuAsnPheLeuLysAspHisPheLeuMetAspGlyGlnVal 379
 QY 1439 TTTCTCTATGAACAAATCGCCCAATAGTATGATCAAAACGGATGTAATATTAATTTACACA 1498
 DB 380 -----ArgSerArgLeuLeuLeuGlnProArgAlaArgTyrGln-----Arg 394
 QY 1499 ATTGCTGTAGACCGAGTGGATGCAGAGATGACAGATGATGATGTTATGTTATCGAACA 1558
 DB 395 ValAlaValHisArgValProGlyLeuHisSerThrTyrAspValLeuPheLeuGlyThr 414
 QY 1559 GATGTTGGGACCGTCTTAAAGTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAA 1618
 DB 415 GlyAspGlyArgLeuHisLysAlaValThrLeuSerSerArgValHis----- 430
 QY 1619 GAGGTTCTCTCGAAGAAATGACAGTTTTTCGGGAACCGACTGCTATTTCAGCAATGGAG 1678
 DB 431 -----IleIleGluLeuGlnIlePheProGlnGlyGlnProValGlnAsnLeuLeu 448
 QY 1679 CTTTCCACTAAGCAGCAACAATATATATTTGTTCAACGGCTGGGGTTCGCCAGCTCCCT 1738
 DB 449 LeuAspSerHisGlyGlyLeuLeuTrpAlaSerSerHisSerGlyValValGlnValPro 468
 QY 1739 TTACACCGGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTGCTCCCGCAGACCTT 1798
 DB 469 ValAlaAsnCysSerLeuTrp---ProThrCysGlyAspCysLeuLeuAlaArgAspPro 487
 QY 1799 TACTGTCTGTGGAGTGTCTGCTGCTG-----TCTCGCTATTTTCCCTGCTGCAAG 1849
 DB 488 TyrCysAlaIleTrpThrGlySerAlaCysArgLeuAlaSerLeuTrpGlnProAspLeuAla 507
 QY 1850 AGACGCAAGACGACAGATATAAGAAATGAGAGACCCACTGACTCAGCTGTTTCAGACTTA 1909
 DB 508 SerArgProTrpThrGlnAspIleGluGlyAlaSerValLysGluLeuCysLysAsn--- 526
 QY 1910 CACCATGATAATCACCATGGCCACAGCCCTGGAAGAGAGATCATCTATGCTGTAGAG--- 1966
 DB 527 -----SerSerTyrLysAlaArgPheLeuValProGlyLysPro 539
 QY 1967 -----AATAGTACACATTTTGGAAATGCAAGTCCGAGTCCGAGTCCG 2002
 DB 540 CysLysGlnValGlnIleGlnProAsnThrValAsnThrLeuAlaCysProLeuLeuSer 559
 QY 2003 CAGAGAGCGCTGCTCTATTGGCAATTTCCAGAGCGCAATGAAAGAGCGAAAGAGATC 2062
 DB 560 AsnLeuAlaThrArgLeuTrpValHisAsnGlyAlaProValAsnAlaSerAlaSerCys 579
 QY 2063 AGAGTGGATGATCATATCATCAGGACAGATCAAGGCTCTCTGCTAGTGTCTTACACAG 2122
 DB 580 ArgVal-----LeuProThrGlyAspLeuLeuValGlySer-----Gln 593
 QY 2123 AAGGATTCAGCAATTACCTCTGCTGCGGTGGACATGCGGTGATCATCAAACTCTTCT 2182
 DB 594 GlnGlyLeuGlyValPheGlnCysTrpSerIleGluGluGlyPheGlnGlnLeuValAla 613
 QY 2183 AAGGTAACCTCGAAGTCAATTCAGCAGAGCATTTTGGAAAGAACTTCTTCAATAAGATGAT 2242
 DB 614 SerTyrCysProGluValMetGlu-----GluGlyValMetAspGlnLysAsn 629
 QY 2243 GATGAGATGGCTCT 2257
 DB 630 GlnArgAspGlyThr 634

RESULT 11
 JC8059
 semaphorin 6D-1 - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 09-May-2004 #sequence_revision 09-May-2004 #text_change 09-May-2004
 C:Accession: Jc8059
 R:Taniguchi, M., and Shimizu, T.
 Biochem. Biophys. Res. Commun. 314, 242-249, 2004
 A:Title: Characterization of a novel member of murine semaphorin family.
 A:Reference number: Jc8059; PMID: 14715272
 A:Accession: Jc8059
 A:Molecule type: mRNA
 A:Residues: 1-1011 <TAN>
 A:Cross-references: DDBJ:AB091532
 C:Comment: This protein is a secreted and transmembrane semaphorin protein belonging to elopment and neuronal plasticity in brain, neurogenesis and morphogenesis, and vasculog
 C:Genetics:
 A:Gene: Sema6D-1
 A:Map position: 2
 C:Keywords: axon guidance; brain; semaphorin; transmembrane protein

Alignment Scores:
 Pred. No.: 1,95e-54 Length: 1011
 Score: 828.00 Matches: 253
 Percent Similarity: 42.89% Conservatives: 133
 Best Local Similarity: 28.11% Mismatches: 236
 Query Match: 16.91% Indels: 218
 DB: 2 Gaps: 40

US-09-774-490-1 (1-2709) x Jc8059 (1-1011)

QY	200	ATGGGCTGTTAACTAGGATTGCTGCTTTCTGGGAGTATTACTTACACAGAGCA	259
DB	1	MetGlyPheLeuLeuLeuTrpPheCysValLeuPheLeuValSerArgLeuArgAla	20
QY	260	AACTATCAGAATGGGAGAACAACTATGCGCCAGGCTGAAATTTATCTACAAAGAAATGTTG	319
DB	21	ValSerPheProGluAsp	27
QY	320	GAATCCCAACAACTGTGATC-----ACTTTCAATGGCTTG	352
DB	28	GluProLeuAsnThrValAspTyrHisTyrSerArgGlnTyrProValPheArgGlyArg	47
QY	353	-----GCCAACAGCTCCATATCATACCTTC-----CTTTGGATGAGGAAGAGT	400
DB	48	ProSerGlyAsnGluSerGlnHisArgLeuAspPheGlnLeuMetLeuLysIleArgAsp	67
QY	401	AGGCTGTATGTCGACCAAGATCACATATTTTCATTCGACTGCTTAATCAAGGAT	460
DB	68	ThrLeuTyrIleAlaGlyArgAspGlnValTyrThrValAsnLeuAsnGluIleProGln	87
QY	461	TTTCAA-----AAGATTGTGTGGCCAGTATCTTACACCAAGAGAGATGAA	505
DB	88	ThrGluValIleProSerLysLysLeuThrTyrArgSerArgGlnGlnAspArgGluAsn	107
QY	506	TGCAAGTGGCTGGAAAGACATCTGGAAGAATGTGCTTAATTCATCAAGTACTTAAG	565
DB	108	CysAlaMetLysGlyLysHis---LysAspGluCysHisAsnPheIleLysValPheVal	126
QY	566	GCATATAATCAGACTCATTGTACGCTGTGGAAGGGGCTTTTCATCCAAATTTGCACC	625
DB	127	ProArgAsnAspGluMetValPheValCysGlyThrAsnAlaPheAsnPrometCysArg	146
QY	626	TACATTGAAATTGGACATCATCTCGAGGCAATATTTTAAAGCTGGAGAACTCACATTTT	685
DB	147	Tyr-----TyrArgLeuArgThrLeuGluTyr	155
QY	686	GAA-----AACGGCGTGGGAAGATGCCATATGACCTTAAGCTGTGACAGCA	733
DB	156	AspGlyGluGluIleSerGlyLeuAlaArgCysProPheAspAlaArgGlnThrAsnVal	175
QY	734	TCCCTTTTATAGATCGAATATATCTCGGAATCTGCACTGATTTATTTGGGGCAGAC	793
DB	176	AlaLeuPheAlaAspGlyLysLeuTyrSerAlaThrValAlaAspPheLeuAlaSerAsp	195
QY	794	TTTGCTATCTTCGAACTCTTGGGCACCACCACCAATCAGGACAGCAGCATGATTC	853

DB	196	AlaValIleTyrArgSerMetGlyAspGlySerAlaLeuArgThrIleLysTyrAspSer	215
QY	854	AGGTGGCTCAATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAACTCT	913
DB	216	LysTrpIleLysGluProHisPheLeu-----HisAlaIleGluTyrGly	230
QY	914	GAAGATGACAAAGATATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGA	973
DB	231	-----AsnTyrValTyrPhePheArgGluIleAlaValGluHisAsnLeuGly	248
QY	974	AAAGCTACTCAGCTAGAAATAGTCATATGCAAGAATGACTTTGGAGGGCACAAGAT	1033
DB	249	LysAlaValTyrSerArgValAlaArgIleCysLysAsnAspMetGlySerGlnArg	268
QY	1034	CTGGTGAATAAA---TGGACAACATTCCTCAAGCTCTCTGATTTGCTCAGTGCCAGT	1090
DB	269	ValLeuGluLysHisTrpThrSerPheLeuLysAlaArgLeuAsnCysSerValProGly	288
QY	1091	CCAAATGGCAATGACACTCATTTGATGAACTGCAG-----GATGATATTCCTAATG	1141
DB	289	AspSerPhePhe-----TyrPheAspValLeuGlnSerIleThrAspIleIleGlnIle	306
QY	1142	AACTTTAAAGATCCTTAAATAATCCAGTTGTATATGAGAGTGTTCACGATTCACGTAACAT	1201
DB	307	Asn-----GlyIleProThrValValGlyValPheThrThrGlnLeuAsnSer	322
QY	1202	TTCAGGATCAGCGCTGTGTATGATAGCTAGTGTGTCAGAGGGTGTCTCTGCT	1261
DB	323	IleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPheLysGly	342
QY	1262	CCATATGCCACAGGATGGACCAACTATCAATGG-----GTCCCTTATCAAGAGAGA	1315
DB	343	ArgPheLysGluGlnLysThrProAspSerValTyrThrAlaValPro---GluAspLys	361
QY	1316	GTCCCTATCCACGGCCAGGAACCTTGTCCAGCAAAACATTTGGT---GGTTTGACTCT	1372
DB	362	ValProLysProArgProGlyCysCysAlaLysHisGlyLeuAlaGluAlaTyrLysThr	381
QY	1373	ACAAAGGACCTTCCTGATGATGTTATACCTTTGCAAGAAGTCATCCAGCCCATGACAT	1432
DB	382	SerIleAspPheProAspAspThrLeuAlaPheIleLysSerHisProLeuMetAspSer	401
QY	1433	CCAGTGTTCCTATCAACAATCGCCCAATAGTATCAAAACGATGTAATATCAATTT	1492
DB	402	AlaValProIleAlaAspGluProTrpPheThrLysThrArgValArgTyrArgLeu	421
QY	1493	ACACAAATGCTGTAGACCGAGTGGATGCAGAAAGATGGACATGATGTTATGTTATC	1552
DB	422	ThrAlaIleGluValAspArgSerAlaGlyProTyrGlnAsnTyrThrValIlePheVal	441
QY	1553	GGACAGATGTTGGACCGCTTCTTAAAGTATTTCAATTCCTAAGGAGACTGGTATGAT	1612
DB	442	GlySerGluAlaGlyValValLeuLysValLeuAla-----LysThrSerProPheSer	459
QY	1613	TTA---GAAGAGTTCGTCTGGAAGAAATGACAGT-----	1648
DB	460	LeuAsnAspSerValLeuLeuGluIleGluAlaTyrAsnProAlaLysCysSerAla	479
QY	1649	-----CGGGAACCGACTGCTATTTCCAGCAATGGAGCTTTCCACTAAGCAGCAACTA	1702
DB	480	GluSerGluGluAspArgLysValValSerLeuGlnLeuAspLysAspHisAlaLeu	499
QY	1703	TATATTTGTTCAACCGCTGGGTTCCCGAGCTCCCTTTACACCGGTGTGATATTTACGG	1762
DB	500	TyrValAlaPheSerCysValValArgIleProLeuSerArgCysGluArgTyrGly	519
QY	1763	AAAGCGTGTGCTGAGTGTTCCTCCCGAGACCTTACTGTGCTTG---GATGTTCT	1819
DB	520	SerCysLysLysSerCysAlaIleAlaSerArgAspProTyrCysGlyTyrLeuSerGlnGly	539
QY	1820	GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCGCAAGACGACAGATATAAGAAAT	1879

Db 540 ValCysGluArgVal-----ThrLeuGlyMetLeuLeuLeuThrGluAspPhe----- 555
 QY 1880 GGAGAGCCCACTGACTGCTTTCAGAGCTTACACCATGATAATCACCAGCCACAGCCCT 1939
 Db 556 -----PheAlaPheHisAsnHisSerPro 563
 QY 1940 -----GAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTTGGAAATGC 1990
 Db 564 GlyGlyTyrGluGlnAspThrGluTyrGly-----AsnThrAlaHisLeuGlyAspCys 581
 QY 1991 AGTCGGAAGTCGAGAGAGCGCTGCTTATGCGCAATTCAGAGCGGGAATAGAGAGCA 2050
 Db 582 HisGly-----ValArgTrpGluValGlnSerGlyGluSerAsnGln 595
 QY 2051 AAAGAAGAGATCAGAGCTG----- 2068
 Db 596 MetValHisMetAsnValLeuLeuThrCysValPheAlaPheValLeuGlyAlaPhe 615
 QY 2069 -----GATGATCATATCATCAGGACAGATCAAGCCCTT 2101
 Db 616 IleAlaGlyValAlaValTyrCysTyrArgAspMetPheValArgLysAsnArgLysIle 635
 QY 2102 CTGCTAGCTAGCTACACAGAGGAT-----TCA 2131
 Db 636 -----HisLysAspAlaGluSerAlaGlnSerCysThrAspSerSer 649
 QY 2132 GGCATATTACTCTGCTCATCGGTGGAAACATGGCTTATACAACTCTTCTTAAGGTAAAC 2191
 Db 650 GlySerPhe-----AlaLysLeuAsnGlyLeuPheAspSerProValLysGluTyr 666
 QY 2192 CTGGAAGTCATTGACACAGAGCATTTG---GAAGAATCTTCTTATAAAGATGATGGA 2248
 Db 667 GlnGlnAsnIleAspSerProLysLeuTyrSerAsnLeu----- 680
 QY 2249 GATGCTCTAAGACCAAGAAATG---TCCATAGCATGACACCTAGCAGAGGTCTGG 2305
 Db 681 -----ThrSerArgLysGluLeuProProAsnThrAspThrLysSerMetAlaValAsp 698
 QY 2306 TACAGA-----GACTTCATGCGAGCTCPC 2329
 Db 699 HisArgGlyClnProGluLeuAlaLeuProThrProGluSerThrProValLeu 718
 QY 2330 AACCAACCCCAATCTCAACAGCATGATGATGTTCTGTGAACAAGTTTGGAAAGG----- 2383
 Db 719 HisGlnLysThrLeuGlnAlaMetLysSerHisSerGluLysAlaHisSerHisGlyAla 738
 QY 2384 GACCGAAAACAAGCTCGGCAA-----AGCCAGGACATACCCCA----- 2422
 Db 739 SerArgLysGluHisProGlnPhePheProSerSerProProHisSerProLeuSer 758
 QY 2422 ----- 2422
 Db 759 HisGlyHisIleProSerAlaIleValLeuProAsnAlaThrHisAspTyrAsnThrSer 778
 QY 2423 ---GGGAACAGTAACAATGGAAGCAGCTTTACAGAAAATAAG----- 2461
 Db 779 PheSerAsnSerAsn-----AlaHisLysAlaGluLysLysLeuGlnSerMetAspHis 796
 QY 2462 -----AAGGTAGAAACAGGAGGACCCAGAAATTTGAGAGGCGACCCAGGAGTGTC 2512
 Db 797 ProLeuThrLysSerSerLysArgGluHisArg-----ArgSerVal 811
 RESULT 12
 148745
 semaphorin B - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 148745
 R:Puschel, A.W.; Adams, R.H.; Betz, H.
 Neuron 14, 941-948, 1995
 A>Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
 A:Reference number: 148744; MUID:95267431; PMID:7748561
 A:Accession: 148745

A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-760 <RES>
 A:Cross-References: UNIPROT:Q62178; EMBL:X85991; NID:g854325; PIDN:CAA59983.1; PID:g854
 C:Genetics:
 A:Gene: semB
 C:Superfamily: semaphorin
 Alignment Scores:
 Pred. No.: 1-72e-52 Length: 760
 Score: 802.00 Matches: 204
 Percent Similarity: 49.32% Conservatives: 122
 Best Local Similarity: 30.88% Mismatches: 251
 Query Match: 16.38% Indels: 84
 DB: 2 Gaps: 23
 US-09-774-490-1 (1-2709) x 148745 (1-760)
 QY 257 GCAAACTATCAGATGGGAAGAACAAATGTGCCAGGCTGAAATATCTTACAAAGAAATGT 316
 Db 30 AlaSerGlyThrGlyGlyGlnGlyProMetProArgValLysTyr-----HisAla 46
 QY 317 TTGGAATCCAAACAATGTGATCATTCTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACC 376
 Db 47 GlyAspGlyHisArgAlaLeuSerPhePheGlnGlnLysGlyLeuArgAspPheAspThr 66
 QY 377 TTCTTTTGGATGAGAACGGAGTAGGTGTATGTTGGAGCAAGAGATCACATATTTTCA 436
 Db 67 LeuLeuLeuSerAspAspGlyAsnThrLeuTyrValGlyAlaArgGluThrValLeuAla 86
 QY 437 TTCGACCTGGTGTAT-----ATCAAGGATTTTCAAAAGATTTGTGGCCCA 481
 Db 87 LeuAsnIleGlnAsnProGlyIleProArgLeuLysAsnMet-----IleProTrpPro 104
 QY 482 GTATCTTACACAGAGAGATGAATGCAAGTGGCTGGNAAGACATCTCTGAAGAAATGT 541
 Db 105 AlaSerGluArgLysThrGluCysAlaPheLysLysLysSerAsnGluThrGlnCys 124
 QY 542 GCTAATTTTCATCAAGGTACTTAAGGCATATATACAGATCACTTGTACCGCTGTGGAACG 601
 Db 125 PheAsnPheIleArgValLeuValSerTyrAsnAlaThrHisLeuTyrAlaCysGlyThr 144
 QY 602 GGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAAATTT 661
 Db 145 PheAlaPheSerProAlaCysThrPheIleGluLeu-----GlnAspSerLeuLeu 161
 QY 662 TTTAAGCTGGAGAACTCATTTTGAAGAGCGCCCTGGGAAGAGTCCATATACCCCTAAG 721
 Db 162 LeuProIleLeuIleAspLysValMetAspGlyLysGlyGlnSerProLeuThrLeuPhe 181
 QY 722 CTGCTGACAGCATCCCTTTTAATAGATGGAATATATCTCTGGAACCTGACGTGATTTT 781
 Db 182 ThrSerThrGlnAlaValLeuValAspGlyMetLeuTyrSerGlyThrMetAsnAsnPhe 201
 QY 782 ATGGGCGGAGACTTTTCTATCTTCGAACTCTTGGGACACCCACCACCAATAGGACAGAG 841
 Db 202 LeuGlySerGluProIleLeuMetArgThrLeuGlySerHisProValLeuLysThrAsp 221
 QY 842 CAGCATGATTCAGGTGGCTCAAT---GATCCAAAGTTTCATTTAGTGGCCCACTCATCTCA 898
 Db 222 IlePhe---LeuArgTrpLeuHisAlaAspAlaSerPheValAlaAla----- 236
 QY 899 GAGAGTGACATCTCTGAGAGATGACAAAGTATATATCTTCTCCGTGAAATCAATAGAT 958
 Db 237 -----IleProSerThrGlnValValTyrPhePheGluGluThrAlaSerGlu 253
 QY 959 GGAGAACACTCTGGAAAGAGCTACTCACGCTAGATAGTGCAGATATGCAAGAAATGACTTT 1018
 Db 254 PheAspPhePheGluGluLeuTyrIleSerArgValAlaGlnValCysLysAsnAspVal 273
 QY 1019 GGAGGGCAGAGAGTCTGCTGATTAATGACAACTTCTCAAGCTCGTCTGATTTGC 1078
 Db 274 GlyGlyGluLysLeuLeuGlnLysLysTrpThrPheLeuLysAlaGlnLeuLeuCys 293

QY 656 -----AATATTTTAAAGCTGGAGAACTCACATTTTGAATAACGCGCTGG----- 700
 Db 161 TyrAlaAsnLeuThrHisLeuProArgSerGluTyrValIleGlyValGlyLeuGlyIle 180
 QY 701 ---AAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAAATAGATGA----- 751
 Db 181 AlaLysCysProIlyrAspProLeuAspAsnSerThrAlaIleTyrValGluAsnGlyAsn 200
 QY 752 -----GAATATATCTCTGGAAGCTGACAGCTGATTTTATGGGCGAGACTTT 796
 Db 201 ProGlyGlyLeuProGlyLeuTyrSerGlyThrAsnAlaGluPheThrLysAlaAspThr 220
 QY 797 GCTATCTTCGAACTCTTGGGACACACCCCAATC----- 832
 Db 221 ValIlePheArgThrAspLeuTyrAsnThrSerAlaLysArgLeuGluTyrLysPheLys 240
 QY 833 AGGACAGAGCAGCATATCCAGCTGCCTCAATGATCCAAAGTTCATTAGTCCACCTC 892
 Db 241 ArgThrLeuLysTyrAspSerLysTrpLeuAspLysProAsnPheValGlySerPheAsp 260
 QY 893 ATCTCAGAGAGTGCACAACTCTGAAGATGACAAAGATATATCTTTCTTCCTCGTCAAAATGCA 952
 Db 261 IleGlyGlu-----TyrValTyrPhePheArgGluThrAla 273
 QY 953 ATAGATGGAGAACACTCTGTGAAAGCTACTACGCTAGATAGTGCAGATATGCAAGAT 1012
 Db 274 ValGluTyrIleAsnCysGlyLysAlaValTyrSerArgIleAlaArgValCysLysLys 293
 QY 1013 GACTTTGGGGGACAGAGTCTGGTGAATAATGACACATCTCTCAAGCTCTCTG 1072
 Db 294 AspValGlyGlyLysAsnLeuLeuAlaHisAsnTrpAlaThrTyrLeuLysAlaArgLeu 313
 QY 1073 ATTTGTCTAGTCCAGCTCCAAATGCGATTCACACTCATTTTGCATCACTGCAGGATGA 1132
 Db 314 AsnCysSerIleSerGlyGlu-----PheProPheTyrPheAsnGluIleGlnSerVal 331
 QY 1133 TTCCTAATGAACCTTTAAAGATCCTAAATAATCCAGTTGTATAGAGTGTTCAGACTTCC 1192
 Db 332 TyrGlnLeuProSerAspLysSerArg-----PhePheAlaThrPheThrThrSer 348
 QY 1193 AGTAACATTTTCAAGGATCAGCGGTGTATGTATAGATGATGATGATGAGAGGGTG 1252
 Db 349 ThrAsnGlyLeuIleGlySerAlaValCysSerPheHisIleAsnGluIleGlnAlaLa 368
 QY 1253 TTCCTTGGTCCATATGCCACAGGATGGACCAACTATCAATGGGTGCT---TATCAA 1309
 Db 369 PheAsnGlyLysPheLysGluGlnSerSerSerAsnSerAlaTrpLeuProValLeuAsn 388
 QY 1310 GGAAGAGTCCCTTATCCAGCGCAGGAACCTGTCCAGCAAAACATTTGGTGTGTTGAC 1369
 Db 389 SerArgValProGluProArgProGlyThrCys-----ValAsn 401
 QY 1370 TCTAAGAGACCTCTCTGATGATGTATTAACCTTGCAGAGATGATCATCCAGCCATGTAC 1429
 Db 402 AspThrSerAsnLeuProAspThrValLeuAsnPheIleArgSerHisProLeuMetAsp 421
 QY 1430 AATCCAGTGTTCCTATGACATCCGCCAATAGTGTCAAAACGCGATGTAATTATCAA 1489
 Db 422 LysAlaValAsnHisGluHisAsnAsnProValTyrTyrLysArgAspLeu-----Val 439
 QY 1490 TTTTACAAATTTCTCTAGAC-----CGAGTGGATGCGAAGATCGACAGATGATGTTT 1543
 Db 440 PheThrLysLeuValValAspLysIleArgIleAspIleLeuAsnGlnGluTyrIleVal 459
 QY 1544 ATGTTTATCGAAGACAGATGTGGGCGGTCTTTAAAGTAGTTTCAATTCCTAAGAGACT 1603
 Db 460 TyrTyrValGlyThrAsnLeuGlyArgIleTyrLysIleValGln----- 474
 QY 1604 TGTATGATTTAAGAGGTTCTGCTGGAAGAATGACAGTTTTCGG-----GAACCG 1657
 Db 475 TyrTyrArgAsnGlyGluSerLeuSerLysLeuLeuAspIlePheGluValAlaProAsn 494

QY 1658 ACTGCTATTTTCCAGCAATGAGCTTTCCTACTAAGCAGCAACAACATATATATGTTCAACG 1717
 Db 495 GluAlaIleGlnValMetGluIleSerGlnThrArgLysSerLeuTyrIleGlyThrAsp 514
 QY 1718 GCTGGGTTCGCCAGCTCCCTTTTACACCGGTGTGATATTTACGGGAAGCGTGTCTGAG 1777
 Db 515 HisArgIleLysGlnIleAspLeuAlaMetCysAsnArgTyrTrpAspAsnCysPheArg 534
 QY 1778 TGTGCTCTCGCCGAGACCTTACTGTGTCTGGATGGTTCCTGCA-----TGTTCCTCG 1831
 Db 535 Cys-----ValArgAspProTyrCysGlyTyrAspLysGluAlaAsnThrCysArgPro 552
 QY 1832 TATTTTCCCACTGCCAAGAGAGCAGCAGACGACAGATATAGAATGAGACCCACTG 1891
 Db 553 Tyr-----GluLeuAspLeuLeuGlnAspValAlaAsn----- 563
 QY 1892 ACTCACTGTTCAGACTTACACCATGATATACCATGGCCACAGCCCTGAAGAGAAATC 1951
 Db 564 ---GluThrSerAspIleCysAspSer-----ValLeuLysLysLysIle 578
 QY 1952 ATC-----TATGGTGTAGAGAAATAGTACACATTTTTCGAATGCGAGTCCGAGTCCGAG 2005
 Db 579 ValValThrTyrGly-----GlnSerValHisLeuGlyCysPheValLysIlePro 595
 QY 2006 AGAGCGCTG-----GTCTATTGGCAATTCACAGGCGGAATGAAGAGCAAAA 2053
 Db 596 GluValLeuLysAsnGluGlnValThrTrp---TyrHisHisSerLysAspLysGlyArg 614
 QY 2054 GAAGAGATCAGAGTGGAT-----GATCATATCATCAGACACAGATCAAGCCCTTCGTCTA 2107
 Db 615 TyrGluIleArgTyrSerProThrLysTyrIleGluThrThrGluArgGlyLeuValVal 634
 QY 2108 COTAGTCTACAACAGAGGATTCAGGCAATTCCTCTGCCAT 2149
 Db 635 ValSerValAsnGluAlaAspGlyArgTyrAspCysHis 648

RESULT 14
 JH0798
 fasciclin IV precursor - American bird grasshopper
 C:Species: Schistocerca americana (American bird grasshopper)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: JH0798
 R:Kolodkin, A.; Mathes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Goo
 A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance i
 A:Reference number: JH0798; PMID:93040225; PMID:1418998
 A:Accession: JH0798
 A:Molecule type: mRNA
 A:Residues: 1-730 <KOL>
 A:Cross-references: UNIPROT:Q26473; GB:I00709; NID:g160844; PID:g160845
 A:Experimental source: embryo
 C:Comment: This protein plays a role in growth cone guidance in the developing central
 C:Keywords: glycoprotein; transmembrane protein
 F;1-2/Domain: signal sequence #status predicted <SIG>
 F;23-730/Product: fasciclin IV #status predicted <MAT>
 F;23-627/Domain: extracellular #status predicted <EXT>
 F;628-652/Domain: transmembrane #status predicted <TM>
 F;653-730/Domain: intracellular #status predicted <INT>
 F;44,71,63,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 8,27e-50 Length: 730
 Score: 766.50 Matches: 209
 Percent Similarity: 47.70% Conservative: 112
 Best Local Similarity: 31.05% Mismatches: 225
 Query Match: 15.66% Indels: 127
 DB: 2 Gaps: 29

US-09-774-490-1 (1-2709) x JH0798 (1-730)

QY 209 TTAACTAGGATGCTGTCTTTCTGGGAGTAGTATTACTTACAGCAAGCAACTATCAG 268
 Db 5 LeuValAlaValAlaAlaLeuLeuTrp---ValAlaLeuHisAlaAla----- 20

A:Residues: 1-656 <KOL>
 A:Cross-references: GB:I26082
 C:Genetics:
 A:Gene: sema1
 A:Cross-references: FlyBase:FBgn0011259

Alignment Scores:
 Pred. No.: 3,61e-47 Length: 656
 Score: 731.50 Matches: 199
 Percent Similarity: 46.92% Conservative: 129
 Best Local Similarity: 28.47% Mismatches: 248
 Query Match: 14.94% Indels: 123
 DB: 2 Gaps: 24

US-09-774-490-1 (1-2709) x B49423 (1-656)

QY 536 GAATGTCCTAATTTTCATCAAGTACTTAAGGCATATAATCAGACTCACTTGTACGCCTGT 595
 DB 3 AspCysGlnAsnTyrIleArgIleMetValValProSerProGlyArgLeuPheValCys 22
 QY 596 GGAACGGGGCTTTTCATCCAATTGC---ACCTACATTGAAATTGGACATCATCCTGAG 652
 DB 23 GlyThrAsnSerPheArgProMetCysAsnThrTyrIle-----IleSer 37
 QY 653 GACAATATTTTAAGCTGAGAACTCACATTTTGAACGGCGCTGGGAGAGTCCATAT 712
 DB 38 AspSerAsnTyrThrLeuGluAlaThr-----LysAsnGlyGlnAlaValCysProTyr 55
 QY 713 GACCTTAAGCTGACAGCATCCCTTTTAATAGATGGAGAATTATACCTCTGGAACCTGCA 772
 DB 56 AppProArgHisAsnSerThrSerValLeuAlaAspAsnGluLeuTyrSerGlyThrVal 75
 QY 773 GCTGATTTTATGGGGCGAGACTTGTCTATCTTCGGAACCTCTTGGGCACCAACCACCAATC 832
 DB 76 AlaAspPheSerGlySerAspProIleIleTyrArg-----GluProLeu 90
 QY 833 AGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTCATTAGTCCCACTC 892
 DB 91 GlnThrGluGlnTyrAspSerLeuSerLeuAsnAlaProAsnPheValSerPhe---- 109
 QY 893 ATCTCAGAGTGCACAACTCCTGAAGATGACAAAGTATACCTTTTCTTCGTTGAAATGCA 952
 DB 110 -----ThrGlnGlyAspPheValTyrPhePheArgGluThrAla 123
 QY 953 ATAGATGGAGAACACTCTCGAAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAT 1012
 DB 124 ValGluPheIleAsnCysGlyLysAlaIleTyrSerArgValAlaArgValCysLysTyr 143
 QY 1013 GACTTTGGAGGACAGAGTCTGGTGAATAATGACAAACATTCCTCAAGCTCTCTG 1072
 DB 144 AspLysGlyGlyProHisArgPheArgAsnArgTyrThrSerPheLeuLysSerArgLeu 163
 QY 1073 ATTTGCTCAGTGCAGGTCCAAATGCGCATGTGACACTCATTTCATCAACTGAGGATGTA 1132
 DB 164 AsnCysSerIleProGly-----AspTyrProPheTyrPheAsnGluIleGlnSerAla 181
 QY 1133 TTCCTAATG-----AACTTTAAAGATCCTTAAATAACCCAGTTCTATATGAGTGT 1183
 DB 182 SerAsnLeuValGluGlyGlnTyrGlySerMetSerSerLysLeuIleTyrGlyValPhe 201
 QY 1184 ACAGCTTCAGTAAACATTTTCAAGGATCAGCGGTGTGTATGATATGATGATGATG 1243
 DB 202 AsnThrProSerAsnSerIleProGlySerAlaValCysAlaPheAlaLeuGlnAspIle 221
 QY 1244 AGNAGGGTTCCTTGGTCCATATGCCAGGGATGGACCCCACTATCAATGGGTGCT 1303
 DB 222 AlaAspThrPheGluGlyGlnPheLysGluGlnThrGlyIleAsnSerAsnTrpLeuPro 241
 QY 1304 TAT---CAAGGAGAGTCCCTTATCCACGCGCAGGAACTTGTCCCGACGAAAAACATTGGT 1360
 DB 242 ValAsnAsnAlaLysValProAspProArgProGlySerCys----- 255
 QY 1361 GGTTCCTGACTCTCAAAAGGACCTTCCTGATGATGTTTATAACCTTTTCAAGAAATCATCCA 1420

DB 256 ---HisAsnAspSerArgAlaLeuProAspProThrLeuAsnPheIleLysThrHisSer 274
 QY 1421 GCCATGTACAATCCAGTGTTCCTATGACAAATCCCAATAGTATGATCAAAACGAGTGA 1480
 DB 275 LeuMetAspGluAsnValProAlaPhePheSerGlnProIleLeuValArgThrSerThr 294
 QY 1481 AATTATCAATTTTACACAAATTCCTGATAGC---CGAGTGGATGCAGAAATGCAGAC--- 1534
 DB 295 IleTyrArgPheThrGlnIleAlaValAspAlaGlnIleLysThrProGlyGlyLysThr 314
 QY 1535 TATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTAAAGTAGTCTTCAATTCCT 1594
 DB 315 TyrAspValIlePheValGlyThrAspHisGlyLysIleLysSerValAsnAlaGlu 334
 QY 1595 AAGGAGACTGTTGATGAT---TTAGAAGAGTCTTCTGCTGGAAGAATAGACAGTTCG 1651
 DB 335 SerAlaAspSerAlaAspLysValThrSerValValIleGluGluIleAspValLeuThr 354
 QY 1652 GAACCGACTGCTATTTTCAGCAATGGAGCTTTCCTACCTAGCAGCA--- 1696
 DB 355 LysSerGluProIleArgAsnLeuGluIleValArgThrMetGlnTyrAspGlnProLys 374
 QY 1697 -----CAACTATATATTTGTTCAACGCTGGGGTTCGCCAGCTC 1735
 DB 375 AspGlySerTyrAspAspGlyLysIleIleValThrAspSerGlnValAlaIle 394
 QY 1736 CTTTACACCGGTGT---GATATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGA 1792
 DB 395 GlnLeuHisArgCysHisAsnAspLysIleThrSerCysSerGluCysValAlaLeuGln 414
 QY 1793 GACCTTACTGTCTGGATGCTGTGCA-----TGT----- 1825
 DB 415 AspProTyrCysAlaTrpAspLysIleAlaGlyLysCysArgSerHisGlyAlaProArg 434
 QY 1826 -----TCTCGCTATTTT-----CCC 1840
 DB 435 TrpLeuGluAsnTyrPheTyrGlnAsnValAlaThrGlyGlnHisAlaLysPro 454
 QY 1841 ACTGCAAGAGAGACGACAGACAGCAAGATATAAGAAATGGAGACCCACTGACTCTGT 1900
 DB 455 SerGlyLysIleAsnSerLys-----AspAlaAsnAlaGlyGlyLysGlyPheArg 472
 QY 1901 TCAGCTTACCATCATGATTAATCAGCATGGCCACAGCCCTGAGAGAGATCATCTATGT 1960
 DB 473 AsnAspMetAspLeuAspSerArgArgGlnSerLysAspGlnLysIleAspAsn 492
 QY 1961 GTAGAGATAGTAGCACATTTTGGATGTCAGTCCGAACTCCGAGAGCGCTGCTAT 2020
 DB 493 IleAspLysAsnPheGlu-----GlyProGlnThrSerAlaAspIleIleAsn 508
 QY 2021 TGGCAATTCAGAGCGCAAAATGAAGAGCGAAAGAGAGATCAGATGATGATCATATC 2080
 DB 509 AlaGlnTyr-----ThrValGluThrLeuVal 517
 QY 2081 ATCAGACAGATCAAGGCTTCTGTCTAGTCTTCAACAGAGATTCAGGCAATTC 2140
 DB 518 MetAlaValLeuAlaGlySerIlePheSerLeuLeuValGlyPhePheThrGlyTyrPhe 537
 QY 2141 CTC-----TGGCATCGGTGGACATGGGTTTCATACAACTCTTCTTAAGGTAACC 2191
 DB 538 CysGlyArgArgCysHisLysAspGluAspAsp-----Asn 549
 QY 2192 CTGGAAGTCAATTCACACA-----GAGCATTTGGAAGAACTTCTTCATAAAGATGAT 2245
 DB 550 LeuProTyrProAspThrGluTyrGluTyrPheGluGlnArgGlnAsnValAsnSerPhe 569
 QY 2246 GGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCAGGAGGTCTCG 2305
 DB 570 ProSerSerCysArgIleGlnGluProLysLeuLeuProGlnValGluGluValThr 589
 QY 2306 TACAGAGCTTCATGAGCTCATCAACACCCCACTCTCAACAGTGTGATGTTCTGT 2365

Db 590 TyrAlaGluProValLeuLeuProGlnProProProProAsnLysMet----- 605
 QY 2366 GAACAAGTTTGGAAAAAGGGACCGAAAAACAACGTCGGCAAGGCCAGGACATACCCAGGG 2425
 Db 606 -----HisSerProLys 609
 QY 2426 AACAGTAAACAAATGGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAAACAGGAGGACC 2482
 Db 610 AsnThrLeuArgLysProProMetHisGlnMetHisGlnGlyProAsnSerGluThr 628

Search completed: March 8, 2005, 21:13:45
 Job time : 169.5 secs

GenCore version 5.1.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 8, 2005, 20:54:21 ; Search time 452.5 Seconds
(without alignments)
6131.370 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896
Sequence: 1 aatctttatttattcatgatg.....aggcttttttcttctaataacc 2709

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cn2_1/USPTO spoal_p/US09774490/runat 08032005 140757 14842/app query.fasta_1.2887
-DB=uniprot_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09774490 @CN 1 1 530 @runat 08032005 140757 14842 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4201	85.8	771	1 SM3A_HUMAN	Q14563 homo sapien
2	4057.5	82.9	772	1 SM3A_RAT	Q63548 rattus norv
3	4035.5	82.4	772	1 SM3A_MOUSE	Q08665 mus musculu
4	3784.5	77.3	772	1 SM3A_CHICK	Q90607 gallus gall
5	3609.5	73.7	774	2 Q8JW9	Q8jiw9 xenopus lae
6	3207.5	65.5	778	1 S3AB_BRARE	Q9w686 brachydanio
7	3075.5	62.8	860	1 S3AA_BRARE	Q9w7j1 brachydanio
8	2258	46.1	777	2 Q8BH34	Q8bh34 m mus muscu
9	2252	46.0	777	2 Q8BMF6	Q8bm6 mus musculu
10	2247.5	45.9	777	1 SM3D_HUMAN	Q95025 homo sapien
11	2245.5	45.9	777	2 Q6UW77	Q6uw77 homo sapien
12	2245	45.9	761	1 SM3D_CHICK	Q90663 gallus gall
13	2125	43.4	764	1 SM3D_BRARE	Q9w696 brachydanio
14	2118	43.3	749	1 SM3B_HUMAN	Q13214 homo sapien
15	2059.5	42.1	748	1 SM3B_MOUSE	Q62177 mus musculu
16	2044	41.7	775	1 SM3E_HUMAN	Q15041 homo sapien

17	2030	41.5	775	2	Q9QX23	Q9qx23 mus musculu
18	2020	41.3	775	1	SM3E_MOUSE	P70275 mus musculu
19	2008.5	41.0	685	2	Q66KH4	Q66kh4 xenopus lae
20	2005.5	41.0	756	2	Q8QGU9	Q8qgu9 gallus gall
21	1993	40.7	785	1	SM3E_CHICK	Q42237 gallus gall
22	1940	39.6	785	1	SM3F_HUMAN	Q13275 homo sapien
23	1928	39.4	785	1	SM3F_MOUSE	Q88632 mus musculu
24	1894	38.7	751	1	SM3C_CHICK	Q42236 gallus gall
25	1862.5	38.0	751	2	Q6NXW7	Q6nxw7 mus musculu
26	1850.5	37.8	751	1	SM3C_MOUSE	Q62181 mus musculu
27	1849.5	37.8	751	1	SM3C_HUMAN	Q99585 homo sapien
28	1830	37.4	782	2	Q9NS98	Q9ns98 homo sapien
29	1765.5	36.1	725	2	Q7L9D9	Q7l9d9 homo sapien
30	1668	34.1	695	2	Q6DFQ0	Q6dfq0 xenopus tro
31	1662	33.9	591	2	Q75M97	Q75m97 homo sapien
32	1653	33.8	695	2	Q6PF60	Q6pf60 xenopus lae
33	1639	33.5	301	2	Q8GJ2	Q8gj2 homo sapien
34	1606	32.8	574	2	Q6ZQD8	Q6zqd8 mus musculu
35	1570	32.1	287	2	Q75MQ2	Q75mq2 homo sapien
36	1516.5	31.0	573	2	Q6P151	Q6p151 homo sapien
37	1271.5	26.0	268	2	Q9HBR1	Q9hbr1 oryzias lat
38	1176.5	24.0	457	2	Q9HBR1	Q9hbr1 homo sapien
39	1139.5	23.3	403	2	Q8BKQ6	Q8bkq6 mus musculu
40	1080	22.1	296	2	Q9J129	Q9j129 rattus norv
41	1048.5	21.4	830	2	Q6NRA4	Q6nra4 xenopus lae
42	1010	20.6	861	2	Q6GTM9	Q6gtm9 mus musculu
43	1003	20.5	861	1	SM4D_MOUSE	Q09126 mus musculu
44	981.5	20.0	862	1	SM4D_HUMAN	Q92854 homo sapien
45	976.5	19.9	799	2	Q8BJC1	Q8bjc1 mus musculu

ALIGNMENTS

RESULT 1
SM3A_HUMAN
ID SM3A_HUMAN STANDARD; PRT; 771 AA.
AC Q14563;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
GN Name=SEMA3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=94094332; PubMed=8269517;
RA Kolodkin A.L., Matthes D.J., Goodman C.S.;
RT "The semaphorin genes encode a family of transmembrane and secreted growth cone guidance molecules..";
RL Cell 75:1389-1399(1993).
RN [2]
RP SEQUENCE OF 1-37 FROM N.A.
RA Woessner J., Minx P., Hinds K., Stromatt C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE OF 39-182 FROM N.A.
RA Rohlfing T., Tin-Wollam A.M., Duckels G.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth cones. Could serve as a ligand that guides specific growth cones by a motility-inhibiting mechanism. Binds to the complex neuropilin-1/plexin-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy third of the protein.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 Sema domain.

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CC or send an email to license@isb-sib.ch).

DR EMBL; L26081; AAG5938.1; -;
DR EMBL; AC004451; RA000353.1; -;
DR EMBL; AC004848; AAC78622.1; -;
DR PIR; D49423; D49423.
DR Genbank; HGNC:10723; SEMA3A.
DR MIM; 603961; -;
DR GO; GO:0005576; C:extracellular; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; SEMA.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF01403; SEMA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; SEMA; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS51004; SEMA; 1.
KW Developmental protein; Glycoprotein; Immunoglobulin domain;
KW Multigene family; Neurogenesis; Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 771 Semaphorin 3A.
FT DOMAIN 31 514 SEMA.
FT DOMAIN 580 664 IG-like C2-type.
FT DOMAIN 727 769 Arg/Lys-rich (basic).
FT DISULFID 649 722 By similarity.
FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 590 590 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 771 AA; 88889 MW; 9985F8D3EAD8456 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x SM3A_HUMAN (1-771)

QY 200 ATGGCTGGTTAACTAGGATCTGCTCTTTCTGGGGAGTATTACTTACAGCAAGACA 259
DB 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGCAACATGTGCCAAGCTGAAATATCTTACAAAGAAATGTG 319
DB 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTC 379
DB 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACGGAGTAGGCTGTATGTGGAGCAAGAGTACATATTTTCATTC 439
DB 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAAATCAAGATTTTCAAAAGATTGTGGCCAGTATCTTACACCAAGACA 499
DB 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAGACATCCTGAAAGATGTGCTAATTTTCATCAAGGTA 559
DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120

QY 560 CTTAAGGCATATAATCAGACTCAGCTGTGTACGCTGTGGAACGGGGCTTTTCATCAATT 619
DB 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGAAATTTGGACATCATCTCAGAGCAATATTTTAAGCTGGAGACTCA 679
DB 141 CysThrTyrIleGluIleGlyHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGCTCAGACGATCCCTT 739
DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATTTACTCTCTGGAAGTGCAGCTGATTTTATGGGCGGAGACTTCT 799
DB 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTGGGCACACACCAATCAGGACAGAGCAGCATGATTCAGGTGG 859
DB 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTTCATTAGTGCCACCTCATCTCAGAGAGTGACAATCCTCAAGAT 919
DB 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTCCGTCAAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979
DB 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTACCGTGAATAGGTGAGATGCAAGAAATGATCTTTGGAGGCGCAGAGTCTGGTG 1039
DB 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATCGCAACATCTCCTCAAGCTCGTCTGATTTCTCAGTCCAGGTCCTCAATGCG 1099
DB 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCTATTTTGATGAACTGAGGATGTATTCTTAATGAACTTTAAAGATCCTAAA 1159
DB 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCAGTTGTATATGGAGTGTTCAGACTCTTCAGTAACATTTTCAAGGATCAGCGTG 1219
DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATATCAGTATGATGTGAGAGGTTCTTCTTGGTCCATATGCCCCACAGGAT 1279
DB 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCCCTATCCAGGCCAGGAACT 1339
DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACCAAAACAAATTTGGTGGTTTGTCTCTCAAAAGGACCTTCTCTGATGATGTTATA 1399
DB 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAGTCCAGCCCATGATCAATCCAGTGTTCCTTATGAACAATCGCCCA 1459
DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGGATGTAATTTATCAAAATTTTACAAAATTTGCTGAGCCAGTGGAT 1519
DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleValAspArgValAsp 440
QY 1520 GCAGAGATGAGCAGTATGATGTTTATCGGAACAGATGTTGGGAGCCCTTCTTAAA 1579
DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATCTTAAAGGAGTGTGATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
DB 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluGluMet 480

QY 1640 ACAGTTTTTCGGGAACCGCTGCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 501 LeuTyrlleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGAAGAACGCTGCTGAGTGTTCCTCGCCCGCAGACCTTACTGTCTGGATGCTTCT 1819
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpaspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTCCTCCACTGCAAGAGACGCAAGACGCAAGATATAAGAAAT 1879
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAen 560
 QY 1880 GGAGACCCACTGACTCAGTTCAGACTTACACCATGATTAATCACCATGCCACACCCCT 1939
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTAGCACATTTTGGATGCGAGTCCGAG 1999
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGACGCTGCTGCTATTGGCAATTCAGAGCGCAATCAAGAGCAAAAGAAGAG 2059
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
 QY 2060 ATCAGAGTGCATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTATCAAA 2119
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGATTTCAGGCAATTAACCTGCTCCATGCGTGGAACTGGTTCATACAACTCTT 2179
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGTAAACCTGGAAGTCAATTCAGCAGAGCAATTTGGAAGAACTTCTTCAAGAT 2239
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
 QY 2240 GATGATGGAGATGGCTTAAGACCAAGAAATGTCCATAGTATGACACCTAGCCAGAG 2299
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 QY 2300 GTCTGTACAGAGATTCATGCTGAGCTCATCAACCCCACTCAACACGATGATGAG 2359
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
 QY 2360 TTCTGTGAACAAGTTTGGAAAAGGACCCGAAACCAACGTCGCAAGGCGCAGCATACC 2419
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgArgGlnArgProGlyHisThr 740
 QY 2420 CAGGGAAACAGTAACAAATGGAAGCAGCTTACAGAAATATAAGAAAGGTAGAAACAGGAGG 2479
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 QY 2480 ACCCAGGAATTCAGAGGCGCCCGAGGAGTCTC 2512
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2

SM3A_RAT
 ID SM3A_RAT STANDARD; PRT; 772 AA.
 AC Q63548;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III).
 GN Name:Sema3a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;

Alignment Scores:

Pred. No.:	0	Length:	772
Score:	4057.50	Matches:	740
Percent Similarity:	98.58%	Conservative:	21
Best local Similarity:	95.85%	Mismatches:	10
Query Match:	82.87%	Indels:	1
DB:	1	Gaps:	1

[1]
 SEQUENCE FROM N.A.
 STRAIN=Wistar; TISSUE=Brain;
 MEDLINE=97073089; PubMed=8915837;
 DOI=10.1002/(SICI)1096-9861(19961118)375:3<378::AID-CNE3>3.0.CO;2-#;
 Giger R.J., Wolfier D.P., De Wit G.M.J., Verhaagen J.;
 "Anatomy of rat semaphorin III/collapsin-1 mRNA expression and
 relationship to developing nerve tracts during neuroembryogenesis.";
 J. Comp. Neurol. 375:378-392(1996).
 RL - FUNCTION: May be involved in guiding growing axons towards their
 targets by forming a molecular boundary that instructs axons to
 engage in the formation of specific nerve tracts. Binds to
 neuropilin.
 CC - SUBCELLULAR LOCATION: Secreted (By similarity).
 CC - DEVELOPMENTAL STAGE: At E11, expression was restricted to the
 olfactory pit, the basal and rostral surface of the telencephalic
 vesicle, the eye anlage, the epithelium of rathe's pouch, and
 somites. At later developmental stages, it was widely distributed
 in neuronal as well as in mesenchymal and epithelial structures
 outside the nervous system. After birth, mesenchymal levels
 decreased rapidly and expression became restricted to specific
 sets of neurons in the CNS. In the mature CNS, it is detectable in
 mitral cells, neurons of the accessory bulb and cerebral cortex,
 cerebellar purkinje cells, as well as a subset of cranial and
 spinal motoneurons.
 CC - DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 third of the protein.
 CC - SIMILARITY: Belongs to the semaphorin family.
 CC - SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC - SIMILARITY: Contains 1 Sema domain.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, X95286; CAA64607.1; -;
 DR RGD; 3657; Sema3a.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 DR PROSITE; PSS1004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal.
 FT SIGNAL 1..20 Potential.
 FT CHAIN 21..772 Semaphorin 3A.
 FT DOMAIN 31..514 Sema.
 FT DOMAIN 577..665 Ig-like C2-type.
 FT DOMAIN 728..770 Arg/Lys-rich (basic).
 FT DISULFID 650..723 By similarity.
 FT CARBOHYD 53..53 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 125..125 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 591..591 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 772 AA; 88808 MW; 240907812FF9F2D2 CRC64;

US-09-774-490-1 (1-2709) x SM3A_RAT (1-772)	Db	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp	360
200 ATGGGCTGGTTAACTAGGATGCTGTCTTTCTGGGAGTATTACTTACAGCAAGCA	QY	1280	GGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCACGGCAGAACT	1339
1 MetGlyTrpPheThrGlyIleAlaCysLeuPheTrpGlyIleLeuLeuThrAlaArgAla	Db	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG	QY	1340	TGTCCACGAAAAAANTTTGGTGGTTTGTCTCTCAAAAGGACCTTCTCGATGATGTTATA	1399
21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLeuLeuSerTyrLysGluMetLeu	Db	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle	400
320 GAATCCAAAGTGTGATCTCTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCCTTC	QY	1400	ACCTTTGCAAGAGTCATCCAGCCATGACCAATCCAGTGTTCCTATGAACATCGCCCA	1459
41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe	Db	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArgPro	420
380 CTTTGGATGAGGAACGGAGTAGCTGTATGTTGGAGCAAGGATCAATATTTTCATTC	QY	1460	ATAGTGATCAAAACCGGATGTAATATCAATTTTACAAATTTGTCTGAGACCGAGTGGAT	1519
61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	Db	421	IleMetIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGCA	QY	1520	GCAGAAGATGACAGTATGATGTTTATCGGAAACAGATGTTGGGACCGTCTTTAAA	1579
81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	Db	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
500 GATGAATGCAAGTGGCTGGAAAGACATCCTGAAAGATGCTTAATTTTCATCAAGGTA	QY	1580	CTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTCTCGAAGAAATG	1639
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	Db	461	ValValSerValProLysGluTrpHisAspLeuGluGluValLeuLeuGluMet	480
560 CTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCCATCCAATT	QY	1640	ACAGTTTTTCCGGAAACCGACTGCTATTTTCCAGCAATGGAGCTTTCACATAAGCAGCAACA	1699
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	Db	481	ThrValPheArgGluProThrThrIleSerAlaMetGluLeuSerThrLysGlnGln	500
620 TGCACTACATTAATGGAATTCGACATCATCTCGAGGCAATATTTTAAAGTCGGAAGACTCA	QY	1700	CTATATATTGTTCAACGGCTGGGTTGCCACGCTCCCTTTTACACCGGTGATATTTAC	1759
141 CysThrTyrIleGluValGlyHisHisProGluAspAsnIlePheLysLeuGlnAspSer	Db	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
680 CATTTTGAAACGGCGTGGAGAGTCCATATGACCCCTAAGCTGTGACAGATCCCTT	QY	1760	GGGAAGCGTGTCTGAGTGTGCTCGCCGAGACCTTACTGCTTGGATGGTGTCT	1819
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	Db	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
740 TTAATAGATGGAATTAATCTCTGAACTGCGAGCTGATTTTATGGGGAGACTTGTCT	QY	1820	GCATCTTCTCGCTATTTTCCCACTGCAAGAGACGACACAAGACGACAAGATAAAGAAAT	1879
181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	Db	541	SerCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn	560
800 ATCTTCCGAACCTTTGGGCACCACCAACCAATCAGACAGACAGCATGATTTCCAGGTGG	QY	1880	GGAGACCACTGACACTGTTTCAGACTTA---CACCATGATAATCACCATGCCACACGC	1936
201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp	Db	561	GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnHisGlyHisSer	580
860 CTCATGATGCAAGTTTCAATGTCGCCACCTCATCTCAGAGAGTGACAATCCTGAGAT	QY	1937	CCTGAAGAGAGAAATCATCTATGCTGAGAGATAGTACACATTTTTCGAATGCAGTCCG	1996
221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp	Db	581	LeuGluGluLysGlyIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro	600
920 GACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAGCT	QY	1997	AACTCCGACAGAGCGCTGCTCTATTGGCAATTTCCAGAGCGCAAAATGGAAGCGAAAGAA	2056
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGlyHisSerGlyLysAla	Db	601	LysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluAspArgLysGlu	620
980 ACTCAGCTAGATAGTCTAGATATCAAGATGACTTTGGAGGGCAGCAAGTCTGGTG	QY	2057	GAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTCTA	2116
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	Db	621	GlulIleArgValGlyAspHisIleIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu	640
1040 AATAAGTGAACAATCTCTCAAGCTCGTCTGATTTGTCAGTGCAGGTCCAAATGGC	QY	2117	CAACAGAGGATTCAGGCAATTTACCTCTGCCATCGGTGGACATGGGTTCATACAACT	2176
281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	Db	641	GlnLysLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheMetGlnThr	660
1100 ATTGACACTCATTTCATGCACTGCAAGATGATTCCTAATGAACCTTAAAGATCCTAAA	QY	2177	CTTCTTAAGGTAAACCTCGAAGTCAATGACACAGAGCATTTTGGGAAGAACTTCTTCATAAA	2236
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnSerLysAspProLys	Db	661	LeuLeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLys	680
1160 AATCAAGTTGTATATCGAGTGTTTTACGATCTTCAGTAAACATTTTCAAGGGATCAGCCGTG	QY	2237	GATGATGATGAGATGGCTCTTAAGCAACCAAGAAATGTCCATAGCATGACCTAGCCAG	2296
321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	Db	681	AspAspAspGlyAspGlySerLysThrLysGluMetSerSerSerMetThrProSerGln	700
1220 TGTATGTATAGCATGATGTGAGAAGGGTGTCTTCTGGTCCATATGATCCCAACAGGAT	QY	2297	ANGTCTCGTACAGAGATTCATGTCAGCTCATCAACCCCACTCAACTCTCAACAGTGGAT	2356
	Db	701	LysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp	720

QY 2357 GAGTTCGTGAACAAGTTTGGAAAGGACCGGAAACAAACAGTCGCGAAAGCCAGGACAT 2416
 |||||
 Db 721 GiuPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHis 740
 |||||
 QY 2417 ACCCCAGGACAGTAAACAAATGGAAGCAGCTTACAGAAATAAGAAAGGTAGAACAGG 2476
 |||||
 Db 741 SerGlnGlySerAsnLysTrpLysHisMetGlnGluSerLysGlyGlyArgAsnArg 760
 |||||
 QY 2477 AGGACCCAGCAATTTGAGAGGCGCCAGGAGTGTC 2512
 |||||
 Db 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772
 |||||
 RESULT 3
 SM3A_MOUSE
 ID SM3A_MOUSE STANDARD; PRT; 772 AA.
 AC 00865; Q62215;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 3A precursor (Semaphorin III) (Sema III) (Semaphorin D) (Sema D).
 GN Name=Sema3a; Synonyms=SEMA3, SemD;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NR1; TISSUE=Embryo;
 RX MEDLINE=95267431; PubMed=7748561; DOI=10.1016/0896-6273(95)90332-1;
 RA Puschel A.W., Adams R.H., Betz H.;
 RT "Murine semaphorin D/collapsin is a member of a diverse gene family
 and creates domains inhibitory for axonal extension.";
 RL Neuron 14:941-948(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97470885; PubMed=9331345; DOI=10.1016/S0896-6273(00)80368-2;
 RA Taniguchi M., Yuasa S., Fujisawa H., Naruse I., Saga S., Mishina M.,
 RA Yagi T.;
 RT "Disruption of semaphorin III/D gene causes severe abnormality in
 peripheral nerve projection.";
 RL Neuron 19:519-530(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Kimura T., Fishman M.C.;
 RT "cDNA sequence of mouse collapsin/semaphorin III.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ Databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McQuinn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]

RP SEQUENCE OF 107-772 FROM N.A.
 RX TISSUE=Fetal brain;
 RC MEDLINE=95267432; PubMed=7748562; DOI=10.1016/0896-6273(95)90333-X;
 RA Messersmith E.K., Leonardo E.D., Shatz C.J., Tessier-Lavigne M.,
 RA Goodman C.S., Kolodkin A.L.;
 RT "Semaphorin III can function as a selective chemorepellent to pattern
 sensory projections in the spinal cord.";
 RL Neuron 14:949-959(1995).
 CC -!- FUNCTION: Plays a role in growth cones guidance. May function to
 pattern sensory projections by selectively repelling axons that
 normally terminate dorsally.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DEVELOPMENTAL STAGE: Expressed early in embryonic development
 (E11) in distinct regions of the neuroectoderm and mesoderm.
 CC Expression became more extensive at later stages.
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X85993; CAA59895.1; -;
 DR EMBL; D85028; BAAL9773.1; -;
 DR EMBL; L41541; AAL7761.1; -;
 DR EMBL; BC057588; AAH57588.1; -;
 DR EMBL; L40484; AAA73934.1; -;
 DR PIR; I48747; I48747;
 DR PIR; I58169; I58169.
 DR MGD; MGI:107558; Sema3a.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; igf.1.
 DR Pfam; PF01403; Sema; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS51004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 772 Semaphorin 3A.
 FT DOMAIN 31 514 Sema.
 FT DOMAIN 579 665 Ig-like C2-type.
 FT DOMAIN 728 770 Arg/Lys-rich (basic).
 FT DISULFID 650 723 By similarity.
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 193 193 D -> N (in Ref. 5).
 FT CONFLICT 207 207 H -> D (in Ref. 1).
 FT CONFLICT 253 253 D -> G (in Ref. 1).
 FT CONFLICT 352 352 F -> L (in Ref. 5).
 FT CONFLICT 403 403 A -> G (in Ref. 1).
 FT CONFLICT 571 572 QH -> ED (in Ref. 1).
 FT CONFLICT 616 620 EDRKE -> RRSKR (in Ref. 1).
 FT CONFLICT 623 623 R -> K (in Ref. 5).
 SQ SEQUENCE 772 AA; 88799 MW; E89A0852B10AEC3 CRC64;
 Alignment Scores:
 Pred. No.: 0 Length: 772
 Score: 4035.50 Matches: 737
 Percent Similarity: 98.32% Conservative: 22
 Best Local Similarity: 95.47% Mismatches: 12
 Query Match: 82.42% Indels: 1
 DB: 1 Gaps: 1

US-09-774-490-1 (1-2709) x SM3A_MOUSE (1-7772)

QY 200 ATGGGCTGTTAACTAGGATGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259
 Db 1 MetGlyTrpPheThrGlyIleAlaCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
 QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATATCTCTACAAAGAAATGTG 319
 Db 21 AsnTyrAlaAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
 QY 320 GAATCCAAATGTGATCACTTTCAATGCTTGGCCAAACAGCTCAGATTATCATCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 QY 380 CTTTGGATGAGAAAGGAGTGGTGTATGTTGGAGCAAGATCACATATTTTCATTC 439
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTTAATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAAGA 499
 Db 81 AsnLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
 QY 500 GATGAATGCAATGGGCTGGAAAAGACATCTCTGAAGATGTGCTAAATTTTCATCAAGTGA 559
 Db 101 AspGluCysLeuTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTAGCTGTGGAAACGGGGCTTTTCATCAAT 619
 Db 121 LeuGluAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTTGAATGGACATCATCTCTGAGCAATATTTTAAAGTGGAGAACTCA 679
 Db 141 CysThrTyrIleGluValGlyHisProGluAspAsnIlePheLysLeuGlnAspSer 160
 QY 680 CATTTTGAACCGGCTGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGATTAATCTCGAAGTGGAGTGTATTTATGGGGAGACTTTGCT 799
 Db 181 LeuIleAspGlyLeuLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCCGAACTCTTGGGACCAACCAATCAGACAGACAGCATGATTCAGAGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCATGATCCAAAGTATATGATGCTCCACCTCATCTCAGAGAGTACATCTGAGAT 919
 Db 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATATCTTTCTCGTGAAATGCAATAGATGGAGAACACTCTGAAAGCT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGATAGTATGATATGCAAGAATGACTTTGGAGGGCAGCAAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAATGGAACAATCTCCTCAAGCTCGTCTGATTTGCTCAGTGCAGGCTCAAAATGGC 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTCATCACTGAGGATGATTTCTTAATGAACCTTAAAGATCTATAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnSerLysAspProLys 320
 QY 1160 AATCCAGTGTATATGAGTGTATGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219
 Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGTGAGAGAGGCTTCTTGGTCCATATGCCCAACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360

QY 1280 GGACCCAACTATCAATGGTGCCTTTATCAAGGAAGAGTCCCTATCCACGCCAGAACT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCACAGAAAACATTTGGTGGTTTACCTCTACAAAGGACCTTCTCTGATGATTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAAGAAGTCATCCAGCCATGACCAATCCAGTGTTCCTATCAACATCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAAACGGATGTAATTTATCAATTTTACAAAATTTGTCGTAGACCGAGT 1519
 Db 421 IleMetIleLysThrAspValAsnTyrGlnPheThrGlnIleValIleAspArgValAsp 440
 QY 1520 GCAGAAGATGACAGATGATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGAGTTCCTGTGGAAGAAATG 1639
 Db 461 ValValSerValProLysGluThrTrpHisAspLeuGluValLeuLeuGluGluMet 480
 QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTTACCAATGGAGCTTTCACATAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrThrIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTTGGTTCAACGGCTGGGTGCTCCAGCTCCCTTTACACCGGTGATATTTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAAGCTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGATGCTTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATCTTCTCGCTATTTTCCCACTCAAGAGAGACGACACAGCAAGATATAAGAAAT 1879
 Db 541 SerCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1936
 Db 561 GlyAspProLeuThrHisCysSerAspLeuGlnHisHisAspAsnHisHisGlyProSer 580
 QY 1937 CCTGAAGAGAGATCATCTATGCTGTAGAGATAGTAGACATTTTGGAAATGCACTCG 1996
 Db 581 LeuGluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 600
 QY 1997 AAGTCGACAGAGCGCTGCTTATTTGGCAATTCAGAGCGCAATTAAGAGCGCAAGAA 2056
 Db 601 LysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluAspArgLysGlu 620
 QY 2057 GAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTA 2116
 Db 621 GluIleArgMetGlyAspHisIleIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu 640
 QY 2117 CAACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGCGGTTCATACAACT 2176
 Db 641 GlnLysLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheMetGlnThr 660
 QY 2177 CTTCTTAAGTAAACCTCGGAGTCAATTCACACAGAGCATTTTCGAAGAATCTTCTTCAAAA 2236
 Db 661 LeuLeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLys 680
 QY 2237 GATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAG 2296
 Db 681 AspAspAspGlyAspGlySerLysIleLysGluMetSerSerSerMetThrProSerGln 700
 QY 2297 AAGTCTGTGTACAGAGACTTCATGAGCTCATCAACCCCACTCATCAACAGATGGAT 2356
 Db 701 LysValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp 720

QY 2357 GAGTCTGTGCAACAGTTTGGAAAGCGGACCGAAACACAGCTCGGCAAGGCCAGGACAT 2416
 |||||
 Db 721 GluPheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHis 740
 |||||
 QY 2417 ACCCCAGGGAACAGTAAACAAATGGAACACTTACAAGAAATAAGAAAGTGAACACAGG 2476
 ::|||
 Db 741 SerGlnGlySerSerSerSerLysTrpLysHisMetGlnGluSerLysLysGlyArgAsnArg 760
 |||||
 QY 2477 AGGACCACGAATTTGAGAGGGCACCAGAGGTGTC 2512
 |||||
 Db 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772

RESULT 4

SM3A_CHICK
 ID SM3A_CHICK STANDARD; PRT; 772 AA.
 AC Q90607;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 3A precursor (Collapsin-1) (COLL-1).
 GN Names=SEMA3A; Synonyms=COLL1;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 322-329; 362-372; 395-403 AND 666-680.
 RC TISSUE=Brain;
 RX MEDLINE=94006554; PubMed=8402908;
 RA Luo Y., Rable D., Raper J.A.;
 RT "Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.";
 RL Cell 75:217-227(1993).
 CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth cones. Could serve as a ligand that guides specific growth cones by a motility-inhibiting mechanism. Binds to neuropilin.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed at relatively high levels in brain and muscle, moderate levels in lung, bursa, and heart and virtually absent in liver. Collapsin-1, -2, -3, and -5 bind to overlapping but distinct axon tracts.
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.

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 CC -----

CC EMBL: U02528; AAC59638.1; --
 CC PIR: A49069; A49069.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR007110; Ig-like.
 CC InterPro: IPR003659; plexin-like.
 CC InterPro: IPR002165; plexin_repeat.
 CC InterPro: IPR001627; Sema.
 CC Pfam: PF00047; Ig; 1.
 CC DR PIR: A49069; A49069.
 CC DR InterPro: IPR003599; Ig.
 CC DR InterPro: IPR007110; Ig-like.
 CC DR InterPro: IPR003659; plexin-like.
 CC DR InterPro: IPR002165; plexin_repeat.
 CC DR InterPro: IPR001627; Sema.
 CC DR Pfam: PF00047; Ig; 1.
 CC DR SMART: SM00403; Sema; 1.
 CC DR SMART: SM00409; IG; 1.
 CC DR SMART: SM00423; PSI; 1.
 CC DR SMART: SM00630; Sema; 1.
 CC DR PROSITE: PS50835; IG LIKE; 1.
 CC DR PROSITE: PS51004; SEMA; 1.
 CC DR Developmental protein; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin domain; Multigene family; Neurogenesis; Signal.

FT SIGNAL 1 22 Potential.
 FT CHAIN 23 772 Semaphorin 3A.
 FT DOMAIN 31 514 Sema.
 FT DOMAIN 576 665 IG-like C2-type.
 FT DOMAIN 728 770 Arg/Lys-rich (basic).
 FT DISULFID 650 723 By similarity.
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 125 125 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 591 591 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 772 AA; 88867 MW; E91E09DE0CC940AC CRC64;

Alignment Scores:

Pred. No.: 8,74e-297 Length: 772
 Score: 3784.50 Matches: 683
 Percent Similarity: 95.34% Conservative: 53
 Best Local Similarity: 88.47% Mismatches: 35
 Query Match: 77.30% Indels: 1
 DB: 1 Gaps: 1

US-09-774-490-1 (1-2709) x SM3A_CHICK (1-772)

QY 200 ATGGGCTGTTAACTAGGATTCTGTCTTTCTGGGAGTATTACTTACAGCAAGCA 259
 |||||
 Db 1 MetGlyTrpLeuArgGlyIleAlaLeuLeuSerLeuGlyValLeuLeuAlaGlyArgVal 20
 |||||
 QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319
 |||||
 Db 21 AsnCysGlnHisValLysAsnValProArgLeuLeuLeuSerTyrLysGluMetLeu 40
 |||||
 QY 320 GAATCCACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATCTTC 379
 |||||
 Db 41 GluSerAsnAsnIleValAsnPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
 |||||
 QY 380 CTTTGGATGAGCAGCGAGTAGGTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
 |||||
 Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 |||||
 QY 440 GACCTGGTTTAATCAAGGATTTTCAAAGATTTGTGTGCCAGTATCTTACACCAGAAGA 499
 |||||
 Db 81 AsnLeuValAsnIleLysGluTyrGlnLysIleValTrpProValSerHisSerArgArg 100
 |||||
 QY 500 GATGAATGAAGCTGGCTGGAAAGACATCTCTGAAGAAGATGCTTAATTTTCATCAAGTTA 559
 |||||
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuArgGluCysAlaAsnPheIleLysVal 120
 |||||
 QY 560 CTTAAGGCATATAATCAGACTCCTGTACGCTGTGGAACGGGGCTTTTCATCAAT 619
 |||||
 Db 121 LeuLysThrTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProMet 140
 |||||
 QY 620 TGCACCTACATTAATGGAATTCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
 |||||
 Db 141 CysThrTyrIleGluValGlySerHisProGluAspAsnIlePheArgMetGluAspSer 160
 |||||
 QY 680 CATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739
 |||||
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 |||||
 QY 740 TTAATAGATGGAGAAATTATCTCTGAACTGAGCTGATTTTATGGGGAGACTTTGCT 799
 |||||
 Db 181 LeuValAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 |||||
 QY 800 ATCTTCCGAACCTCTTGGGCACCACCAATCAGGACAGACAGCATGATTCACGGTGG 859
 |||||
 Db 201 IlePheArgThrLeuGlyHisHisIleProLysIleArgThrGluGlnHisAspSerArgTrp 220
 |||||
 QY 860 CTCATATGATCCAAAGTTCATTAAGTCCACCTCATCTCTCAGAGAGTGACAATCTGAAGAT 919
 |||||
 Db 221 LeuAsnAspProArgPheIleSerAlaHisLeuIleProGluSerAspAsnProGluAsp 240
 |||||
 QY 920 GACAAAGTATATCTTTCTTCGTTGAAATGCAATAGATGGAGACACTCTGGAAGCT 979
 |||||
 Db 241 AspLysIleTyrPhePheArgGluAsnAlaIleAspGlyGluHisThrGlyLysAla 260

QY 980 ACTCAGCTAGTAATAGGTGAGATATGCAAGAAATGACTTTGGAGGCGCACAGAACTGTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGACAAATCTCTAAAGCTGCTGATTTGCTAGTGCAGGTCCAAATGGC 1099
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTGATGAACCTGAGGAGTATTCCTAATCAATTTAAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGlnLeuGlnAspValPheLeuMetCAsnSerLysAspProLys 320
 QY 1160 AATCAGTGTGATATGAGAGTGTTCAGACTTCAGCTTAACATTTTCAAGGGATCAGCCGTG 1219
 Db 321 AsnProIleValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGGGAT 1279
 Db 341 CysMetTyrSerMetThrAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAGAGTCCCTATCCAGCGCCAGGAAT 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTTGGTGGTTCGACTCTCAAAAGGAGCTTCCTGATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspGluValIle 400
 QY 1400 ACTTTGCAAGAGTCATCCAGCCATGTACATTCAGTGTTCCTATGAACTACGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnSerArgPro 420
 QY 1460 ATAGTCATCAAAACCGATTAATATCAATTTACACAAATGTCTGAGACCGAGTGGAT 1519
 Db 421 IleMetIleLysThrAspValAspTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 CGAAGATGAGCAGTATGATGTTATGTTTATCGGAACAGATGTGGACCGCTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspIleGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATGTATGAGAGGTTCTGCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrTrpHisGluLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTCGGGACCGACTGCTATTTCAGCAATGGAGCTTTCACATAAGCAGCAACAA 1699
 Db 481 ThrValPheArgGluProThrValIleSerAlaMetLysIleSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCAACGGCTGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
 Db 501 LeuTyrIleGlySerAlaThrGlyValSerGlnLeuProLeuHisArgCysAspValTyr 520
 QY 1760 GGGAAAGCTGTGCTGAGTGTGCTGCTGCGCAGACCTTACTGTGCTTGGATGTTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGTATTTTCCCTCTGCAAGAGCGCACAGACGACACAGATATAGAAAT 1879
 Db 541 SerCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTCACTGTTTCAGACTTAA---CACCATGATAATCACCATGCCACAGC 1936
 Db 561 GlyAspProLeuThrHisCysSerAspLeuGlnHisAspAsnProSerGlyGlnThr 580
 QY 1937 CCTGAAGAGAGATCATCTATGCTGTAGAGATATAGTAGACATTTTGGAAATCGATCCG 1996
 Db 581 LeuGluGluLysIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerPro 600
 QY 1997 AGTCCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATCAAGAGCGCAAGAA 2056
 Db 601 LysSerGlnArgAlaIleValTyrTrpGlnPheGlnLysGlnAsnAspHisVal 620
 QY 2057 GAGATCAGAGTGTGATCATATCATCATCAGACAGATCAAGGCGCTTCTGCTACGTAGTCTA 2116

Db 621 GluIleLysValAspArgMetIleArgThrGluGlnGlyLeuLeuLeuArgSerLeu 640
 QY 2117 CAACAGAGGATTTCAGGCAATTTACCTCTGCATCGGTGGGAACATGGGTTCATACAACT 2176
 Db 641 GlnArgArgAspSerGlyIleTyrPheCysHisAlaValGluHisGlyPheIleGlnThr 660
 QY 2177 CTTCCTTAAGGTAACCTCGAAGTTCATTCACACAGACGATTTTGGAAAGAACTTCTTCATAA 2236
 Db 661 LeuLeuLysValThrLeuGluValIleAspThrAspHisLeuGluGluLeuHisLys 680
 QY 2237 GATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATCAGCTAGCCAG 2296
 Db 681 GluGluAspAlaAspAlaSerLysThrLysAspAlaThrAsnSerMetThrProSerGln 700
 QY 2297 AAGTCTCTGTCACAGAGCTTCATGCAGCTCATCACACCCCAATCTCAACACGATGGAT 2356
 Db 701 LysIleTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAsp 720
 QY 2357 GAGTCTCTGTAACAAAGTTTGGAAAGGACCGAAGCAACAACTCGGCAAGGCCAGACAT 2416
 Db 721 GluPheCysGluGlnValTyrLysArgAspArgLysGlnArgGlnArgProAlaAsn 740
 QY 2417 ACCCCAGGGAACAGTAACAATGGAGCATTACAGAAATATAGAAAGGTAGAAACAGC 2476
 Db 741 AlaGlnValAsnThrAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760
 QY 2477 AGGACCCACGATTTGAGAGGCGCCACAGGAGTGTC 2512
 Db 761 ArgThrHisGluPheGluArgAlaProArgSerVal 772

RESULT 5
 QBJW9
 ID Q8JW9 PRELIMINARY; PRT; 774 AA.
 AC Q8JW9;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Semaphorin 3A.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head;
 RA Tannahill D., Nielsen J., Regan A.G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY030051; AAK38166.1; -.
 DR HSSP; Q92854; 1OLZ.
 DR GO; GO:0016020; C.membrane; IEA.
 DR GO; GO:0004872; F.receptor activity; IEA.
 DR GO; GO:0007275; P.development; IEA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR001005; Myb DNA binding.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF01437; PSI; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR PROSITE; PS00037; MYB 1; UNKNOWN 1.
 SQ SEQUENCE 774 AA; 89319 MW; 3127FD2E0CDD5FA4 CRC64;

Alignment Scores: 1.228-282 Length: 774
 Pred. No.: 3609.50 Matches: 654
 Score:

Percent Similarity:	93.67%	Conservative:	71
Best Local Similarity:	84.50%	Mismatches:	46
Query Match:	73.72%	Indels:	3
DB:	2	Gaps:	3
US-09-774-490-1 (1-2705) x Q8JW9 (1-774)			
QY	200	ATGGGCTGGTTAACTAGGATTGTCTCTCTTTCTGGGGAGTATTACTTACAGCAGAGCA	259
DB	1	MetGlySerLeuThrTrpIleAlaPheLeuPheLeuGlyValSerLeuThrThrArgLeu	20
QY	260	AACTATCAGAATGGGAAGAACATGTGCCAAGSCTGAAATATCTACAAAGAAATGTG	319
DB	21	AsnCysGlnAsnValLysAsnAsnValProArgLeuArgLeuSerTyrLysGluMetVal	40
QY	320	GAATCCAAACATGTGATCTTCAATGGCTTGGCCCAACAGCTCCAGTATTATCACTTTC	379
DB	41	GluSerAsnAsnLeuIleThrPheAsnGlyTrpProAsnSerSerSerTyrAsnThrPhe	60
QY	380	CTTTGGATGAGAACGGAGTAGGCTGTATGTGGAGCAAGATCACATATTTTCATTC	439
DB	61	ValLeuAspGluGlyArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGTTAATATCAAGATTCTCAAAAGATTGTGCGCCAGTATCTTACACCAAGA	499
DB	81	AsnLeuAlaAsnValLysGluPheGlnLysIleLeuTrpProValThrAsnIleArgArg	100
QY	500	GATGAATGCAAGTGGCTCGAAAAGACATCCCTGAAAGATGTGCTAAATTTTCATCAAGT	559
DB	101	AspGluCysLeuTrpAlaGlyLysAspIleValLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACTGTAGCTGTGGAAACGGGGCTTTTCATCCAATT	619
DB	121	LeuLysAlaTyrAsnHisThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProVal	140
QY	620	TGCACCTACATTGAAATGGACATCATCTCTGAG---GACAAATTTTAAAGCTGAGAAC	676
DB	141	CysThrTyrIleAspValGlyHisTyrProGluGlnAspAsnValPheLysLeuGluAsp	160
QY	677	TCACATTTTGAACCGCGTGGGAAGAGTCCATATGACCCTAAGCTGCTGACACATCC	736
DB	161	SerPhePheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSer	180
QY	737	CTTTTAATAGATGGAATATTATCTCTGGAATCGAGCTGATTTTATGGGGCAGACTTT	796
DB	181	IleLeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPhe	200
QY	797	GCTATCTCCGAATCTTGGGCACACACCCCAATCAGGACAGACAGATGATTCAGG	856
DB	201	AlaIlePheArgThrLeuGlyAsnHisHisProIleArgThrGluGlnHisAspSerArg	220
QY	857	TGGCTCAATGATCCAAAGTTTATTAGTGCACCTCATCTCAGAGAGTGACAAATCCTGAA	916
DB	221	TrpLeuAsnAspProArgPheIleGlyAlaTyrLeuValProGluSerAspAsnProGlu	240
QY	917	GATGACAAAGTATCTTTTCTCCGTGAAATAGCAATAGATGGAGAACACTCTCGAAAA	976
DB	241	AspAspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisThrLysLys	260
QY	977	GCTACTCAGCTAGATAGGTGAGATATGCAAGATGATTTTGGAGGGCAGCAAGATCTG	1036
DB	261	AlaThrHisAlaArgIleGlyGlnLeuCysLysAsnAspPheGlyGlyHisArgSerLeu	280
QY	1037	GTGAATATGACACATCTCTCAAGCTCTGATTTGCTGATTTGCTGATGCTGAGTCAAT	1096
DB	281	ValAsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsn	300
QY	1097	GGCATTGACACTCATTTTTCATCACTGCAAGATGTATTCTCAATCAACTTTTAAAGATCT	1156
DB	301	GlyIleAspThrHisPheAspGluLeuGlnAspValValLeuMetAsnSerLysAspPro	320
QY	1157	AAAAATCCAGTTGTATATGGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGGATCAGCC	1216

DB	321	LysAsnProValValTyrAlaValPheThrThrSerSerAsnIlePheLysGlySerAla	340
QY	1217	GTGTGTATGTATAGCATGATGATGAGAGGGTGTCTCTTGGTCCATATGCCACACAGG	1276
DB	341	ValCysMetTyrSerLeuThrAspIleArgValPheLeuGlyProTyrAlaHisArg	360
QY	1277	GATGACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCGCAGA	1336
DB	361	AspGlyProAsnTyrGlnTrpValProPheGlnGlyArgValProTyrProArgProGly	380
QY	1337	ACTTCTGCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGAGCTTCTCTGATGAT	1396
DB	381	ThrCysProArgGlnThrPheGlyGlyPheAspSerThrLysAspLeuProAspGluVal	400
QY	1397	ATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCGC	1456
DB	401	IleMetPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsnArg	420
QY	1457	CAATAGTGTATCAAAACCGGATGTAATATCAATTTTACAAATTTGCTAGACCGAGTG	1516
DB	421	ProIleIleIleLysThrGluValAspTyrGlnPheThrGlnIleValValAspArgVal	440
QY	1517	GATGCAGAAGTGGACAGTATGATGTTATCGGAACAGATGTTGGGACCGTCTT	1576
DB	441	GluAlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspMetGlyThrIleLeu	460
QY	1577	AAAGTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAA	1636
DB	461	LysValValSerValProLysGluThrTrpThrAspLeuGluGluValLeuLeuGluGlu	480
QY	1637	ATGACAGTTTTCGGGAACCGACTGCTATTTACAGCAATGGAGCTTTCACTAAGCAGCAA	1696
DB	481	MetThrValPheArgGluProThrAlaIleSerAlaMetGluIleSerThrLysGlnGln	500
QY	1697	CAACTATATATGTTTCAACGGCTGGGCTGCCAGCTCCCTTTTACCGGCTGATATT	1756
DB	501	GlnLeuTyrIleGlySerSerValGlyValSerGlnLeuProLeuHisArgCysAspVal	520
QY	1757	TACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCCCTTACTGTGTTGGATGCT	1816
DB	521	TyrGlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGly	540
QY	1817	TCTGCATGTTCTCGCTATTTTCCCACTCCAAGAGACGCCAAGACGACAGATATAAGA	1876
DB	541	SerSerCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArg	560
QY	1877	AATGAGACCCACTGACTCAGTCTGCTCAGACTTA---CACCATGATATCACCATGCCAC	1933
DB	561	AsnGlyAspProLeuThrHisCysSerAspLeuGlnHisGlnAspAspProHisArgGln	580
QY	1934	AGCCTGAAGAGAGAACTCATCTATGCTGAGAGAACTAGCACATTTTGGAAATGCAGT	1993
DB	581	SerLeuGluGluLysIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSer	600
QY	1994	CCGAAGTCCGACAGAGCGCTGCTTATTGGCAATTTCCAGAGCGCAAAATGAGAGCAAAA	2053
DB	601	ProLysSerGlnArgAlaLeuValPheTrpGlnPheGlnLysGlnAsnGluGluLysLys	620
QY	2054	GAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGT	2113
DB	621	AspGluIleLysValAspGluArgLysIleLysThrGluHisGlyLeuLeuArgThr	640
QY	2114	CTACAAGAAGGATTTCAGGCAATTTACCTCTGCCATCGGTGGACATGGGTTCATACAA	2173
DB	641	LeuLysLysArgAspSerGlyIleTyrTyrCysAsnAlaValGluHisGlyPheMetGln	660
QY	2174	ACTCTTCTTAAGTAACCTCGAAATCATTCACACAGAGCATTTTGGAAAGAACTTCTCAT	2233
DB	661	ThrLeuLeuLysValThrLeuGluIleIleAspThrGluHisLeuAspGluLeuLeuHis	680
QY	2234	AAAGATGATGAT---GGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACCT	2290
DB	681	LysGluAspGluGlyGlyAspSerHisLysHisLysGluProSerAsnSerMetSerPro	700

QY 2291 AGCCAGAAAGGCTGTGATACAGACATTCATGACGCTCATCAACCCCAATCTCAACAG 2350
 Db 701 ThrGlnLysIleTrrTyArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThr 720
 QY 2351 ATGGATAGTCTGTGAACAAGTTGGGAAAGGACCGGAAACACAGCTGCGCAAGGCCA 2410
 Db 721 MetAspGluPheCysGluGlnValTrrLysArgAspArgLysGlnArgArgGlnLysAsn 740
 QY 2411 GCACATACCCAGGACAGTAAACAAATGGAGCACTTACAGAAATAGAAAGGTAGA 2470
 Db 741 GlyAsnValGlnValSerAsnThrLysTrrLysHisLeuGlnGluAsnLysLysGlyArg 760
 QY 2471 AACAGGAGGACCCACAAATTCAGAGGCGCACCCAGGAGTGC 2512
 Db 761 AsnArgArgThrHisGluPheGluArgAlaProArgSerVal 774

RESULT 6
 S3AB BRARE
 ID S3AB BRARE STANDARD; PRT; 778 AA.
 AC Q9W686;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 3ab precursor (Semaphorin 1B) (Semaphorin 21B) (Sema-21B).
 GN Name=sema3ab; Synonyms=sema21b;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99425174; PubMed=10495275; DOI=10.1016/S0925-4773(99)00153-7;
 RA Roos M., Schachner M., Bernhardt R.R.;
 RT "Zebrafish semaphorin 21b inhibits growing motor axons in vivo.";
 RL Mech. Dev. 87:103-117(1999).
 CC -!- FUNCTION: Might normally influence the midsegmental pathway choice
 CC of the ventrally extending motor axons by contributing to a
 CC repulsive domain in the posterior somite.
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in rhombomeres three and five, and
 CC in the posterior half of newly formed somites which is avoided by
 CC ventrally extending motor axons.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF083382; RAD28103.1; -;
 CC ZFIN; ZDB-GENE-991209-6; sema3ab.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003659; plexin-like.
 CC InterPro; IPR002165; plexin_repeat.
 CC InterPro; IPR001627; Sema.
 CC Pfam; PF00047; Ig; 1.
 CC Pfam; PF01437; PSI; 1.
 CC Pfam; PF01403; Sema; 1.
 CC SMART; SM00409; IG; 1.
 CC SMART; SM00423; PSI; 1.
 CC SMART; SM00630; Sema; 1.
 CC PROSITE; PS50835; IG_LIKE; 1.
 CC PROSITE; PS51004; SEMA; 1.
 CC Developmental protein; Glycoprotein; Immunoglobulin domain;
 CC Multigene family; Neurogenesis; Signal.
 KW

FT SIGNAL 1 17 Potential.
 FT CHAIN 18 778 Semaphorin 3ab.
 FT DOMAIN 32 515 Sema.
 FT DOMAIN 579 668 Ig-like C2-type.
 FT DOMAIN 721 776 Arg/lys-rich (basic).
 FT DISULFID 652 716 By similarity.
 FT CARBOHYD 54 54 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 593 593 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 778 AA; 88904 MW; 4D36F4323AE21895 CRC64;

Alignment Scores:
 Pred. No.: 3,83e-250 Length: 778
 Score: 3207.50 Matches: 591
 Percent Similarity: 84.90% Conservative: 78
 Best Local Similarity: 75.00% Mismatches: 92
 Query Match: 65.51% Indels: 27
 DB: 1 Gaps: 8

US-09-774-490-1 (1-2709) x 83AB_BRARE (1-778)
 QY 200 ATGGGCTGTTAACTAGGATTGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACA 259
 Db 1 MetAspTrrLeuTrrTrpIleValLeuLeuIleTrrThrLeuIleAlaProGluArgGly 20
 QY 260 AACTAT--CAGAATGGGAAGAACAAATGTCCAGGCTGAAATTTATCTCAAAAGAAATG 316
 Db 21 ThrValAlaGlnAtgSerLysSerAsnValProArgLeuLysProSerTrrLysGluMet 40
 QY 317 TTGGAATCCAAATGATGATCACTTTCAATGGCTTGGCAACAGCTCAGTTATCATACC 376
 Db 41 LeuGluSerAsnAsnLeuThrPheAsnGlyLeuAlaAsnSerSerAlaTrrHisThr 60
 QY 377 TTCCTTTTGGATGAGGAACGAGTAGGTGTATGTTGGAGCAAGAAAGATCAACATATTTCA 436
 Db 61 PheLeuLeuAspGluArgGlyArgLeuPheValGlyAlaLysAspHisValLeuSer 80
 QY 437 TTCGACCTGGTTTAATATCAAG---GATTTTCAAAGATTTGTGTGCCAGTATCTTTACACC 493
 Db 81 PheAsnLeuValAspIleAsnMetAspGlnGlnLeuIleSerTrrProSerSerProSer 100
 QY 494 AGAAGATGATGAATGCAATGGCTGGAAAGACATCTCTGAAAGATGCTTAATTTTCATC 553
 Db 101 ArgArgAspGluCysLysTrrPalaGlyLysAspValGlnLysGluCysAlaAsnPheIle 120
 QY 554 RAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCAT 613
 Db 121 LysValLeuGlnProPheAsnGlnThrHisLeuTrrAlaCysGlyThrGlyAlaPheHis 140
 QY 614 CCAATTTTGACCTACATTAATGGAATTCGACATCATCTCGAGGACAATATTTTAAAGCTGGAG 673
 Db 141 ProValCysAlaHisValGluValGlyLysArgSerGluAspAsnThrPheArgLeu--- 159
 QY 674 AACTCAGATTTGAAAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCA 733
 Db 160 GlySerSerPheGluAsnGlyArgGlyLysSerProTrrAspProLysLeuGlnThrAla 179
 QY 734 TCCCTTTTAAATAGATGGGAATTAATCTCTGGAATCGACGCTGATTTTATGGGGCGAGAC 793
 Db 180 SerMetLeuIleAspGlyGluLeuTrrAlaGlyThrSerAlaAspPheMetGlyArgAsp 199
 QY 794 TTTGTCTATCTCCGAACTCTTGGGCAACCAACCAATCAGGACAGAGCAGCATGATCC 853
 Db 200 PheAlaIlePheArgThrLeuGlyLysHisHisProIleArgThrGluGlnHisAspSer 219
 QY 854 AGGTGGCTCAATGATCCAAAGTTCATTAAGTCCCACTCATCTCAGAGAGTCAACATCTCT 913
 Db 220 ArgTrrLeuAsnAspProArgPheValSerValHisLeuIleProGluSerAsnAla 239
 QY 914 GAAGATGCAAAAGTATACCTTTTCTCCGTGAAAATGCAATAGATGAGAGACACACTGGA 973
 Db 240 GluAspAspLysIleTrrLeuPheArgGluAsnAlaIleAspGlyGluGlnIleSer 259

QY 974 AAAGCTACTCAGCTAGATAGTACATATGCAAGAATGACTTTGGAGGCGACAGAAGT 1033
DB 260 LyAlaThrHisAlaArgIleGlyGlnLeuCysLeuAsnAspPheGlyGlyHisArgSer 279
QY 1034 CTGGTGAATAAATGGACAATTCCTCAAGCTCGCTGATTTGCTCAGTGCAGGTCCA 1093
DB 280 LeuValAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerValProGlyLeu 299
QY 1094 AATGGCAATGACACTCATTTTGATGAACCTGCAGGATGTATTCTTAATGAACCTTTAAAGAT 1153
DB 300 AsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeuMetSerLysAsp 319
QY 1154 CCTAAAATCCAGTGTATATGAGTGTTCAGAGTGTTCAGTGTTCAGTGTTCAGGATCA 1213
DB 320 ProLysAsnProIleIleTyAlaValPheThrThrSerSerAsnIlePheLysGlySer 339
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QY 1274 AGGATGGACCCCAACTATCAATGGGTGCCTTATCAAGGAGAGTCCCTTATCCAGCGCA 1333
DB 360 ArgAspGlyProAsnTyrGlnTrpValProPheLeuAsnArgValProTyrProArgPro 379
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DB 380 GlyThrCysProSerLysThrPheAspGlyPheGluSerThrLysAspPheProAspAsp 399
QY 1394 GTTATACCTTTGCAAGAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGACAAAT 1453
DB 400 ValIleThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProIleAsnAsn 419
QY 1454 CGCCCAATAGTCAATAAAGCGATGTAATTTATCAATTTACAAATTTGCTGAGACCGA 1513
DB 420 HisProIleIleIleLysThrAspValAspTyrGlnPheThrGlnIleValValAspArg 439
QY 1514 GTGGATGCAAGATGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1573
DB 440 ValGluAlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspMetGlyThrVal 459
QY 1574 CTTAAAGTAGTTTCAATTCCTAAGGAGATGCTGATGATGATGATGATGATGATGATG 1633
DB 460 LeuLysValIleSerIleProArgGlyThrTrpHisAspLeuGluValLeuLeuGlu 479
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DB 480 GluMetThrValPheArgGluProThrAlaIleThrAlaMetGluLeuSerThrLysGln 499
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DB 500 GlnGlnLeuTyrLeuGlySerAlaIleGlyValSerGlnMetProLeuHisArgCysAsp 519
QY 1754 ATTTAGCGGAACGGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGAT 1813
DB 520 ValTyrGlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAsp 539
QY 1814 GGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1873
DB 540 GlySerGlnCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIle 559
QY 1874 AGAATGGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1930
DB 560 ArgAsnGlyAspProLeuThrGlnCysSerAspLeuGlnHisAspGluAlaAspGly 579
QY 1931 CACAGCCCT---GAAAGAGAAATCATCTATGTTGTAGAGAAATAGTACATTTTGGAA 1987
DB 580 GluAlaGlyLeuLeuAspLysThrValTyrGlyValGluAsnSerSerPheLeuGlu 599
QY 1988 TGCAGTCCGAAGTCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2047
DB 600 CysSerProLysSerGlnArgAlaLeuIleTyrTrpGlnPheGlnArgHisGlyGluAsp 619
QY 2048 CGAAAAAGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2107

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DB 640 ArgSerLeuHisGlnLysAspSerGlyValTyrTyrCysHisAlaValGluHisGlyPhe 659
QY 2168 ATACAACTCTTCTTAAGGTAACCTCGAAGTCAATTCAGACAGAGATTTGGAGAACTT 2227
DB 660 IleGlnThrLeuLeuArgLeuThrLeuAsnValIleProAlaGluHisLeuAspAspLeu 679
QY 2228 CTTTATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2287
DB 680 LeuHisArgAspPro-----ProAspThrAsnAspProAlaAsnGly----- 693
QY 2288 CTTAGCCAGAGCTCTGGTACAGACACTTCATGCTCAGCTCATCAACACCCCAATCTCA 2347
DB 694 -----LysMetTrpTyrArgAspPheLeuSerLeuLeuAsnProProSerProAsn 710
QY 2348 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2407
DB 711 SerValAspGlnLeuCysGluGlnValTrpLysArgLysGlnArgArgGlnLys 730
QY 2408 CCAGCA-----CATACCCCGAGGAC 2428
DB 731 AlaAsnLeuLeuHisAlaSerGlnSerHisThrSerGlnIleLeuHisSerGlnSer 750
QY 2429 AGTAACTAAATGGAAGCAGCTTACAGAAATAAGAAAGGTAGAAACAGAGGAGCCACG 2488
DB 751 HisAlaLysTrpLysLeuLeuGlnGluAsnLysLysGlyArgAsnArgArgThrHisGlu 770
QY 2489 TTTGAGAGCGCCAGGAGTGTCT 2512
DB 771 MetGlnArgAlaProArgSerVal 778
RESULT 7
S3AA BRARE STANDARD; PRT; 860 AA.
ID S3AA BRARE AC Q9W7J1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Semaphorin 3a precursor (Semaphorin 1A) (Semaphorin 21A) (Sema-21A).
GN Name=sema3a; Synonyms=sema3a;
OC Brachydanio rerio (Zebrafish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=99313409; PubMed=10386838; DOI=10.1016/S0361-9230(99)00038-6;
RA Yee C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,
RA Kuwada J.Y.;
RT "Molecular cloning, expression, and activity of zebrafish semaphorin 21A";
RL Brain Res. Bull. 48:581-593(1999).
CC -!- FUNCTION: May influence outgrowth by a variety of growth cones including those of the posterior lateral line ganglion.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- DEVELOPMENTAL STAGE: Expressed in highly specific patterns within the developing embryo.
CC -!- SIMILARITY: Belongs to the semaphorin family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 Sema domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch).

EMBL; AF086761; AA043984.1; -.
ZFIN; ZDB-GENE-991209-3; sema3aa.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin-repeat.
InterPro; IPR001627; Sema.
Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
SMART; SM00630; Sema; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS51004; SEMA; 1.
KW Developmental protein; Glycoprotein; Immunoglobulin domain;
Multigene family; Neurogenesis; Signal.
Potential.
SIGNAL
FT CHAIN
FT CHAIN
FT CHAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DOMAIN
FT DISULFID
FT CARBOHYD
FT CARBOHYD
FT CARBOHYD
FT CARBOHYD
SQ SEQUENCE

Alignment Scores:

Pred. No.:	1.85e-239	Length:	860
Score:	3075.50	Matches:	561
Percent Similarity:	76.73%	Conservative:	105
Best Local Similarity:	64.63%	Mismatches:	97
Query Match:	62.82%	Indels:	105
Gap:	1	Gaps:	6

US-09-774-490-1 (1-2709) x S3AA BRARE (1-860)

Qy		200	ATGGGCTGGTTAACTAGATTGTCTGTCTTTTCTGGGAGTAATACTTACACAAGACGA	259
Dd		1	MetAspTyrLeuValGlyIlePheLeuLeuLeuLeuCysGlyValAlaLeuProGlyArgVal	20
Qy		260	AACATCAGAATGGGAAGAACAACTGTGCCAAGGCTGAATATTCCTACAAAAGAAATGTG	319
Dd		21	AlaProGlnHisThrLysGluAsnValProArgLeuLeuLysLeuSerTyrAsnGluMetLeu	40
Qy		320	CAATCCAAACAATGTGCATCATCTTCAATGGCTTGGCCACACGAGCTCCAGTTTATCATACCTTC	379
Dd		41	GluSerSerAsnLeuValThrPheThrGlyLeuAlaAsnSerSerGlyTyrAspThrPhe	60
Qy		380	CTTTTGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGATCACATAATTTTCATTC	439
Dd		61	LeuMetAspGlyGluArgGlyArgLeuLeuValGlyAlaGluAspHisValPheSerPhe	80
Qy		440	GACTGGTTAATATC---AAGATTTTCAAAGATTGTGGCCAGTACTCTACACCAGA	496
Dd		81	AspLeuValAlaSerAspValLysGlnIleAlaTrpAlaThrProSerLys	100
Qy		497	AGAGATGAATCGAAGTGGCTGGAAAGACATCTTCAAAGATGTGCTAATTTTCATCAAG	556
Dd		101	ArgAspGluCysLeuYrTipAlaGlyLysAspLeuArgLysAspCysSerAsnPheValArg	120
Qy		557	GTACTTAAGGCATATAATCAGACTCACTTGTACGGCTGTGGAAACGGGGCTTTTCATCCA	616
Dd		121	ValLeuGlnSerTyrAsnGlnThrHisIleTyrIleCysGlyThrGlyAlaPheHisPro	140
Qy		617	ATTTCACCTACATGAAATTCGACATCATCTCTGAGGACAATATTTTTTAAGCTGGAGAAC	676
Dd		141	IleCysSerPheLeuGluMetGlyLysArgAlaGluAspAsnIlePheArgLeuAspAla	160
Qy		677	TCACATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTCAAGCTGTGCAGCATCC	736


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Db 574 pVallystrGlyAspProlethrGlnCysTrpAspIleGluAspSerIleSerHis-- 593
QY 1930 CCACAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATATAGTACACATTTTGTGAATG 1989
Db 594 -GluThrAlaAspGluysValIlePheGlyIleGluPheAenSerThrPheLeuGluCy 613
QY 1990 CAGTCCGAGTGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAATGAAGAGCG 2049
Db 613 sIleProLysSerGlnGlnAlaSerValGluTrpTyrlleGlnArgSerGlyAspGluHi 633
QY 2050 AAAAGAAGATGATCAGAGTGGATGATCATATCATCAGCAGATCAAGGCTCTGCTAG 2109
Db 633 sArgGluGluLeuLysProAspGluArgIleLeuLysThrAspTyrglyLeuLeuIleAr 653
QY 2110 TAGTCTACACAGAGATTCAGGCAATTAACCTCTGCCATGGTGGAAATGTCATGGTTCAT 2169
Db 653 gSerLeuGlnLysLysAspSerGlyMetTyrcysLysAlaGlnGluHisThrPheIle 673
QY 2170 ACAAACTCTTCTTAAGTAACTGGAAGTCAATGATGACAGAGCATTTGGAAGACTTCT 2229
Db 673 eHisThrIleValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsn---Th 692
QY 2230 TCATAAAGATGATGATGAGATGGCTTAAGACCAAGAAATGTCATAGCATGACACC 2289
Db 692 rGlnArgAlaGluTyrglnGluGluGlnValLysAspLeuLeuAlaGluSer----- 709
QY 2290 TAGCCAGAAAGTCTGTGACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACAC 2349
Db 710 -----ArgLeuArgTyrlsAspTyrlleGlnIleLeuSerSerProAsnPhe---Se 726
QY 2350 GATGATGATGCTGTGTGAACAAGTTTGGAAAGGACCGAAACCAACGTCGCAAGGCC 2409
Db 726 rLeuAspGlnTyrcysGluGlnMetTrpTyrlsGluLysArgArgGlnArgAsnLys-- 745
QY 2410 AGGACATACCCAGGAGCAAGTAAACAGTGAAGCTTACAGAAATTAAGAAAGTGTAG 2469
Db 746 -----GlySerProLysTrpLysHisMetGlnGluMetLysLysLysAr 760
QY 2470 AAACAGGAGGACCCAC---GAATTTGAGGGGACCCAGGAGTGTCTC 2512
Db 760 gAsnArgArgHisArgAspLeuAspGluLeuGlnArgSerVal 775
RESULT 9
Q8BMF6 PRELIMINARY; PRT; 777 AA.
AC Q8BMF6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo male testis cDNA, RIKEN full-length
DE enriched library, clone:6030494C20 product:SEMAPHORIN 3D homolog.
GN Name=Sema3d;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwaagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK031704; BAC27522.1; --
DR HSP; Q92854; 10LZ.
DR MGD; MGI:1860118; Sema3d.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003659; Plexin-like.
DR InterPro; IPR002165; Plexin_repeat.
DR InterPro; IPR001627; Sema.
DR Pfam; PF01437; PSI; 1.
DR Pfam; PF01403; Sema; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00423; PSI; 1.
DR SMART; SM00630; Sema; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 777 AA; 89562 MW; B7204D82288B89CE CRC64;
Alignment Scores:
Pred. No.: 6,62e-173 Length: 777
Score: 2252.00 Matches: 427
Percent Similarity: 72.11% Conservative: 147
Best Local Similarity: 53.64% Mismatches: 191
Query Match: 46.00% Indels: 31
DB: 2 Gaps: 13
US-09-774-490-1 (1-2709) x Q8BMF6 (1-777)

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 22 pMetLeuIleMetThrValLeuPheLeuProValThrGluThrSer----- 38
 265 TCAGATGGGAGACAACTGTCAGGCTGAAATTCCTCAAGAAATGTTGGAATC 324
 39 -----LysGlnAsnIleProArgLeuLysLeuThrThrLysAspLeuLeuSe 55
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 613 sIleProLysSerGlnGlnAlaSerValGluTrpTyrIleGlnArgSerGlyAspGluHi 633
 2050 AAAAGAGAGATCAGAGTGGATGATCATATCATCAGAGCAGATCAAGGCTTCTGCTAGC 2109
 633 sArgGluLeuLeuLysProAspGluArgIleIleLysThrAspTyrGlyLeuLeuIleAr 653
 2110 TAGTCTCAACAGAGAGATTCAGCAATTAATCTCTGCCATGCGGTGGGAACATGGGTTCAT 2169
 653 gSerLeuGlnLysLysAspSerGlyWetTyrTyrCysLysAlaGlnGluHisThrPheI 673
 2170 ACAAACTCTTCTTAGGTAAACCTCGAAGTCAATTCACAGAGCATTTTGGAGAACTTCT 2229
 673 eHisThrIleValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsn---Th 692
 2230 TCATAAAGATGATGATGAGATGGCTCTAAGACCAAAAGAAATGTCCTCAATAGCATGACAC 2289
 692 rGlnArgAlaGluTyrGlnGluGlyGlnValLysAspLeuLeuAlaGluSer----- 709
 2290 TAGCCAGAGAGGTCTGGTACAGAGACTTCATGAGCTCATCAACACCCCACTCTCAACAC 2349
 709 rGlnArgAlaGluTyrGlnGluGlyGlnValLysAspLeuLeuAlaGluSer----- 709
 2290 TAGCCAGAGAGGTCTGGTACAGAGACTTCATGAGCTCATCAACACCCCACTCTCAACAC 2349

Db 710 -----ArgLeuArgTyrIleGlnIleLeuSerSerProAsnPhe---Se 726
 QY 2350 GATGGATGATCTCTGGAACAAGTTTGGAAAGGCGACGAAACAACACGTCGGCAAGGCC 2409
 Db 726 rLeuAspGlnTyrCysGluGlnMetTrpTyrIleGluGluArgGlnAsnLys-- 745
 QY 2410 AGGACATACCCAGGAAACAGTACAAATGGAAGCACTTACAGAAAATAAGAAAGGTAG 2469
 Db 746 -----GlySerProLysTrpLysHisMetGlnGluMetLysLysLysAr 760
 QY 2470 AAACAGGAGGACCCAC---GAATTTTCAGAGGGCACCCAGGAGTGC 2512
 Db 760 gaenArgArgHisLeuAspLeuAspGluLeuGlnArgSerVal 775

RESULT 10
 SM3D HUMAN STANDARD; PRT; 777 AA.
 ID SM3D HUMAN STANDARD; PRT; 777 AA.
 AC Q95025; O8NC01;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Semaphorin 3D precursor.
 GN Name=SEMA3D;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mead K., Graves T., Wilson C.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 327-777 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Induces the collapse and paralysis of neuronal growth
 cones. Could potentially act as repulsive cues toward specific
 neuronal populations. Binds to neuropilin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- DOMAIN: Strong binding to neuropilin is mediated by the carboxy
 third of the protein.
 CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.

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 or send an email to license@isb-sib.ch)

DR EMBL; AC004957; -; NOT ANNOTATED CDS.
 DR EMBL; BC029590; AAH29590.1; ALT_INIT.
 DR Genew; HGNC:10726; SEMA3D.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR002165; Plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS0835; IG-Like; 1.
 DR PROSITE; PS1004; SEMA; 1.
 KW Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal.
 FT SIGNAL 1 39 Potential.
 FT CHAIN 40 777 Semaphorin 3D.
 FT DOMAIN 44 531 Sema.
 FT DOMAIN 592 680 IG-like C2-type.
 FT DOMAIN 739 773 Arg/Lys-rich (basic).
 FT DISULFID 665 731 By similarity.
 FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 607 607 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 724 724 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 777 AA; 89651 MW; 3F7B0D7AF50F53BD CRC64;

Alignment Scores:
 Pred. No.: 1.53e-172 Length: 777
 Score: 2247.50 Matches: 414
 Percent Similarity: 73.94% Conservative: 142
 Best Local Similarity: 55.05% Mismatches: 175
 Query Match: 45.90% Indels: 21
 DB: 1 Gaps: 10

US-09-774-490-1 (1-2709) x SM3D_HUMAN (1-777)
 QY 275 AAGAACAAATGTCGCAAGCTGAAATATCTCTCAAGAAGAAATGTTGGAATCCAAATGTG 334
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCATGGCTGGCCCAACAGCTCCAGTTATCATCTCTCTTTGGATGAGGAA 394
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu 78
 QY 395 CGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCATCGACCTGGTTAATATC 454
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
 QY 455 ---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACAGAGAGAGATGAATCAAG 511
 Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
 QY 512 TGGGCTGGAAGAGACATCTGAAAGATGTGTAATTTTCATCAAGTACTTAAAGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
 QY 572 ATCACTTTCATCTGTACGCTGTGGAGCGGGGCTTTTCATCCAAATTTGCACCTACAT 631
 Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
 QY 632 GAAATTTGGACATCATCTCCGAGCAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691
 Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178
 QY 692 GCGCTGGGAAGAGTCCATATGACCTACCTAGCTGTCGACAGCATCCCTTTTAAATAGTA 751
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 QY 752 GAAATTTACTCTGGAACTGCACCTGATTTTATGGGCGGAGACTTGTCTCTCCGAAT 811
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218

QY 812 CTTGGG-----CACCACCACCAATCAGGACAGACGATGATTCACAGTGGCTC 862
Db |||||
QY 219 LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrIlePleu 238
Db |||||
QY 863 AATGATCCAAATTCATTAGTCCACCTCATCTCAGAGAGTGAACAATCCTGGAAGTAC 922
Db |||||
QY 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAAGTATATCTTTCTTCGGTGAATAATGCAATAGATGGAGACATCTCGAAGACTACT 982
Db |||||
QY 259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY 983 CACGCTAGATAGTTCAGATATGCAAGATGATCTTTGGAGGACACAGAGTCTGCTGAAT 1042
Db |||||
QY 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACTTCCTCAAGCTCGTCTGATTCTCAGTCCAGGTCCTCAATGGCATT 1102
Db |||||
QY 299 LysTyrThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTTGGTGAAGTGCAGATGTATCTTAATGAATTTAAAGATCCTAAAT 1162
Db |||||
QY 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CCAGTTGTATATGGAGTGTTCACGACTTCCAGTAACTTTTCAAGGATCAGCCGTGT 1222
Db |||||
QY 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGATGAGAGGGTTCCTTGGTCCATATGCCACAGGATGA 1282
Db |||||
QY 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCAACTATCATGGTGCTTATCAAGAAAGTCCCTATCCAGCCGAGACTTGT 1342
Db |||||
QY 379 AlaAspHisArgTyrValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY 1343 CCAGCAAAACATTTGGTGGT---TTTGACTCTCAAAAGGACTTCTCTGATGATGATA 1399
Db |||||
QY 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
QY 1400 ACCTTTGCAAGATCATCCAGCATGTACAAATCCAGTGTTCCTATGAAACATCCGCA 1459
Db |||||
QY 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyPro 438
QY 1460 ATAGTATCAAAACGATGATATATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
Db |||||
QY 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY 1520 GCAGAGATGACAGTATGATGATGTTTATCGGAACAGATGTTGGACCCGTTCTTAA 1579
Db |||||
QY 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGATG 1639
Db |||||
QY 479 ValValSerIleSerLysGluLysTyrPheAsnMetGluGluValValLeuGluLeu 497
QY 1640 ACAGTTTTCGGAACCGACTCTATTTCAGCAATGAGCTTTCCTACTAAGCAGACAA 1699
Db |||||
QY 498 GlnIlePheLysHisSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
QY 1700 CTATATATTTGGTTCAACGCTGGGTGCGGCTCCAGCTCCCTTTTACACGGTGTGATTTAC 1759
Db |||||
QY 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY 1760 GGAAGACGTGTGCTAGTGTTCCTCGCCGAGACCCCTTACTGTCTTGGATGTTCT 1819
Db |||||
QY 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgProTyrCysAlaTyrAspGlyAsn 557
QY 1820 GCATGTTCTCGTATTTTCCACTGCAGAGACGACAGACGACCAAGATATAGAT 1879
Db |||||
QY 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577
QY 1880 GGAGACCCACTGACTGCTTTCAGACTTTACACCATGATTAATCACCATGCCACGCT 1939

Db |||||
QY 578 GlyAspProIleThrGlnCysTyrAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGACAAATCATCTATGCTGTAGAGAAATAGTACCAATTTTGGATTCAGTCCGAG 1999
Db |||||
QY 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCGCAGACAGCGTGTCTATTGGCAATTCAGAGCGCAAAATGAAGAGCAAAAGAG 2059
Db |||||
QY 617 SerGlnGlnAlaThrIleLysTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY 2060 ATCAGAGTGGATCATCATCATCAGACAGACATCAAGCCTTCTCTCTAGTGTACAA 2119
Db |||||
QY 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAAGATTACGCAATTCCTCGCATCGGTGGACATCGGTTTATACAACTCTT 2179
Db |||||
QY 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY 2180 CTTAAGGTAAACCTGGAAGTCTATTGACACAGACAGCATTTTGGAAAGACTTCTT 2239
Db |||||
QY 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGAGATGGCTCTAAGACCAACAAAGAAATGTCCATAGCATGACACCTAGCC 2299
Db |||||
QY 697 His-----GluGluGlyLysValLysAsp-----LeuLeuAlaGluSerArg 710
QY 2300 GTCTGGTACAGAGACTTCATGCTGAGTCTATCAACACCCCAATCTCAACAGTGTGATG 2359
Db |||||
QY 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAAGTTTGGAAAGGACCGAAACAAACGTCGGCAAGGCGAGCATACC 2419
Db |||||
QY 730 TyrCysGluGlnMetTyrPheIleArgGluLysArgGlnArgAsnLysGlyGly 747
QY 2420 CCAGGAAACAGTAAACAAATGGAAGCATTTCAAGAAATAAGAAAGGTAGAAACAGGAG 2479
Db |||||
QY 748 -----ProLysTyrLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCAC---GAATTTGAGGCGCACCCAGGAGTGTCT 2512
Db |||||
QY 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775
RESULT 11
Q6UW77
ID Q6UW77 PRELIMINARY; PRT; 777 AA.
AC Q6UW77;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Collapsin-2.
GN ORFNames=UNQ760;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vanden R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yaneura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358937; AAQ89296.1; -.

Qy	983	CACGCTAGAAATAGGTCAGATATCAAGAATGACTTTGGAGGGCACAGAACTCTGGTGAAT	1042
Db	279	LeuSerArgValGlyArgValCysAsnAspValGlyGlnArgSerLeuIleAsn	298
Qy	1043	AAATGACACAACTCCTCAAAAGTCCTGATTTGCTCAGTGCAGGTCCAAATGCATT	1102
Db	299	LysTrpThrPheLeuIysAlaArgLeuIleCysSerIleProGlySerAspGlyAla	318
Qy	1103	GACACTCATTTTCATGAACTCGAGGATGATTCTTAATGAACCTTTAAAGATCCTAAAAT	1162
Db	319	AspThrTyrrPheAspGluLeuGlnAspIleTyrrLeuLeuProThrArgAspGluArgAsn	338
Qy	1163	CCAGTTGTATATGGAGTGTTCACGCTTCAGTAAACATTTTCAAGGATCAGCCGCTGTGT	1222
Db	339	ProValValTyrrGlyValPheThrThrThrSerSerIlePheIysGlySerAlaValCys	358
Qy	1223	ATGTATAGCATGAGTCGTGACAAGGGTTCCTTGGTCCATATCCCCACAGGATGGA	1282
Db	359	ValTyrrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrrAlaHisIysGluSer	378
Qy	1283	CCCAACTCATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGGCCAGAACTTGT	1342
Db	379	AlaAspHisArgTrpValGlnTyrrAspGlyArgIleProTyrrProArgProGlyThrCys	398
Qy	1343	CCGACGAAAACATTTGGTGGT---TTGACTCTCAAAAGGACCTTCCTGATGATGTATA	1399
Db	399	ProSerLysThrTyrrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
Qy	1400	ACCTTTGCAAGAAGTCATCCAGCCATGTACATCCAGTGTTCCTATGAACAATCGCCCA	1459
Db	419	SerPheIleLysArgHisSerValMetTyrrLysSerValTyrrProValAlaGlyIlePro	438
Qy	1460	ATAGTGATCAAAACGGATGTAATATTCAATTTACACAAATTCGTAGACCCAGATGGAT	1519
Db	439	ThrPheLysArgIleAsnValAspTyrrArgLeuThrGlnIleValValAspHisValIle	458
Qy	1520	GCAGAAAGATGGACAGTATGATGTATTGTTTATCGGAACAGAGATTTGGGACCGTCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
Qy	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGAGTTCTGCTGGGAAGAAATG	1639
Db	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeuLys	497
Qy	1640	ACAGTTTTCGGGAAACCGACTGCTATTTCAGCAATCGAGCTTTCACCTAAGCAGCAACAA	1699
Db	498	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
Qy	1700	CTATATATTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTATC	1759
Db	518	LeuTyrrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyrr	537
Qy	1760	GGGAAACGGTGCTCAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGGTTCT	1819
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrrCysAlaTrpAspGlyIys	557
Qy	1820	GCATGTTCTCGCTATTTCCCATCTGCAAGAGAGACGACAGACAGCAAGATATAAGAAAT	1879
Db	558	AlaCysSerArgTyrrAlaProThrSerLysArgArgAlaArgGlnAspValIysTyrr	577
Qy	1880	GGAGACCCACTGACTCACTGTTCCAGACTTATCACCATGATAATCACCATGCCACAGCCCT	1939
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
Qy	1940	GAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGCAATTTTGGAAATGCAGTCCGAAG	1999
Db	597	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
Qy	2000	TCGCAGAGACGGCTGGTCTATTGGCAATTCAGAGCGGAAATCCAGAGCGGAAAGAGAG	2059
Db	617	SerGlnGlnAlaThrIleLysTrpTyrrIleGlnArgSerGlyAspGluHisArgGluGlu	636

CC -!- SIMILARITY: Belongs to the semaphorin family.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 Sema domain.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AF124485; RAD21310.1; -;
 DR ZFIN; ZDB-GENE-990715-2; sema3d.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003659; Plexin-like.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
 DR PROSITE; PS51004; Sema; 1.
 DR Developmental protein; Glycoprotein; Immunoglobulin domain;
 KW Multigene family; Neurogenesis; Signal.
 FT SIGNAL 1 41
 FT CHAIN 42 764
 FT DOMAIN 48 535
 FT DOMAIN 661 740
 FT DOMAIN 741 762
 FT DISULFID 668 733
 FT CARBOHYD 143 143
 FT CARBOHYD 490 490
 FT CARBOHYD 610 610
 FT CARBOHYD 610 610
 SQ SEQUENCE 764 AA; 87859 MW; A3ED95C2C479D7AE CRC64;

Alignment Scores:

Pred. No.:	1,21e-162	Length:	764
Score:	2125.00	Matches:	390
Percent Similarity:	71.37%	Conservative:	156
Best Local Similarity:	50.98%	Mismatches:	191
Query Match:	43.40%	Indels:	28
DB:	1	Gaps:	11

US-09-774-490-1 (1-2709) x: SM3D_BRARE (1-764)

QY	215	AGCATGCTGCTCTTTCTGGGAGTATTACTTACAGCAAGACCAACTATCAGATGGG	274
DB	20	ArgPheSerCysAlaTrpTrpSerThrSerValMetLeuPhePheSerLeuProGluGly	39
QY	275	-----AAGAACATGTCAGAGCTGAAATATCTACAAAGAAATGTTGGAATCC	325
DB	40	AsnCysMetLysGluSerLeuProArgValLysLeuGlyTyrLysAspLeuLeuHisSer	59
QY	326	AACAATGTGATCACTTCAATGGCTTGGCCACAGCTCCAGTTATCATCTCTCTTTTG	385
DB	60	ArgSerValProPheThrGlySerSerGluGlyGlnHisPheGlnThrValLeuLeu	79
QY	386	GATGAGAACGAGTGGCTGTATGTTGGAGCAAGGATCATATTTTCATTCGACCTG	445
DB	80	AspGluGluArgSerArgLeuLeuGlyAlaLysAspHisValTyrLeuLeuAspPro	99
QY	446	GTTAATATC- -AAGGATTTTCAAAGATGTGTGGCCAGTATCTTACACCAAGAGAT	502
DB	100	AspAsnLeuAsnLysHisProLysLysLeuSerTrpProAlaSerArgAspArgValGlu	119
QY	503	GAATGCAAGTGGCTGGAAAGACATCTCGAAAGATGTGCTAATTTTCATCAAGTACT	562
DB	120	MetCysLeuLeuAlaGlyLysAsnProLeuThrGluCysAlaAsnPheLeuArgValLeu	139
QY	563	AGGCATATATCAGACTTCATGTCGCTGTGGACCGGGCTTTTCATCAATTTGC	622
DB	140	HisSerTyrAsnArgThrHisValTyrAlaCysGlyThrGlyAlaPheHisProThrCys	159

QY	623	ACCTACATTGAAATTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCACA	682
DB	160	AlaPheLeuGluLeuLysGlyHisLysGluAspArgTrpLeuLeuLeuHisSerAsnThr	179
QY	693	TTTGAACACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTA	742
DB	180	MetGluSerGlyArgMetLysCysProAsnGlnProPheAlaSerValLeu 199	
QY	743	ATAGATGAGATATTAATCTCTGGAAGTCTGAGTATTTATGGGCGGAGACTTGTCTATC	802
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QY	803	TTCCCAACTCTTGGG- - - - -CACCACACCAATCAGACAGAGCAGCATGATCC	853
DB	220	ThrArgSerLeuGlyProProHisGlnGlnTyrIleArgThrAspIleSerGluAsp	239
QY	854	AGGTGGCTCAATGATCCAAAGTTCATAGTGCCTCACTCATCTCAGAGAGTGAACATCT	913
DB	240	TyrTrpIleAsnGluGlyLysPheIleSerAlaHisProIleSerAspThrTyrAsnPro	259
QY	914	GAAGATGACAAAGTATCTTTCTCCGTGAAATGCAATAGATGGGAGAACACTCTGA	973
DB	260	AspAspAspLysIleTyrPhePheArgGluAlaSerArgAspGlySerThrThrAsp	279
QY	974	AAAGCTACTCAGCTAGATAGTATGCAATATGCAAGATGACTTTGGAGGGCAGACAAGT	1033
DB	280	LysSerValLeuSerArgValAlaArgIleCysArgAsnAspValGlyGlyLeuArgSer	299
QY	1034	CTGGTGAATAATGACAACTTCTCTAAAGTCTCTGATTTGCTGCTGCTGCTGCTGCTG	1093
DB	300	LeuThrAsnLysTrpThrPheLeuLysAlaArgLeuValCysSerIleProGlyPro	319
QY	1094	ATGCGATTCAGACTCATTTGATGAACTGAGGAGTATTCCTTAATGAACCTTAAAGAT	1153
DB	320	AspGlyValAspThrHisPheAspGluLeuGlnAspIlePheLeuLeuProSerArgAsp	339
QY	1154	CCTAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCAGTAACTATTTCAAGGATCA	1213
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QY	1214	GCCGTGTGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1273
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DB	460	ArgValAlaAlaGluAspGlyGlnTyrAlaValMetPheLeuGlyThrAspMetGlySer	479
QY	1571	GTTCTTAAAGTATTTCAATCTTAAAGGACTTGGTATGATGATGATGATGATGATGATG	1630
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DB	499	GluGluLeuGlnValPheLysAsnProSerProIleLeuAsnMetGluValSerSerLys	518

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 DR GO; GO:0007411; Praxon guidance; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003659; plexin-like.
 DR InterPro; IPR002165; plexin_repeat.
 DR InterPro; IPR001627; Sema.
 DR Pfam; PF00047; IG; 1.
 DR Pfam; PF01403; Sema; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00423; PSI; 1.
 DR SMART; SM00630; Sema; 1.
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 KW Multigene family; Signal.
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 FT DOMAIN 30 513 Sema.
 FT DOMAIN 573 659 Ig-like C2-type.
 FT DOMAIN 699 702 Poly-Gly.
 FT DOMAIN 724 744 Arg-rich (basic).
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 QY 401 AGCGTGTATGGAGCAAGAGTACATATTTTCATTCGACTGGTTAATATC---ARG 457
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 Db 334 GlnGlySerAlaValCysValTyrSerMetAsnAspValArgArgAlaPheLeuGlyPro 353
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 QY 1325 CCACGGCCAGGAACCTTTGCCAGCAAAACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1384
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Job time : 552.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 01:12:06 ; Search time 11629 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: gb_pat.*
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14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2508.4	92.6	2530	6	AX743092 Sequence
4	2508.4	92.6	2530	6	BD084822 Diagnosis
5	2508.4	92.6	2530	9	HUMHSEM
6	2508.4	92.6	2530	11	G31703
7	2508.4	92.6	2601	6	AR040598
8	2508.4	92.6	2601	6	I47054
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13	1909.4	70.5	2319	10	RNSIITCN1
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO0155455.
ACCESSION AX207154
VERSION AX207154.1 GI:15394943
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Jin, S.
TITLE Resistance sequences and uses thereof
JOURNAL Patent: WO 0155455-A 1 02-AUG-2001;
Millennium Pharmaceuticals, Inc. (US) ; Jin, Shengfang (US)
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Db	1	AATCTTTATTTATCGATGTTAAACAAGCTTAGTAAATCGATCCACGTCGAGGGGTGCG	100.0%	2709;	6;	0;	0;	0;	0;
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Db	121	CCAGATTGTTGAACCTTCTTGCGCGCAATACAGGAAGGAAGACTAAAGCAGCAAGG	100.0%	2709;	6;	0;	0;	0;	0;
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Db	181	GACCTACAGCGTCTCAGCATGGGCTGGTTAACTAGGATTGCTGCTTTCTTCTGGGAGT	100.0%	2709;	6;	0;	0;	0;	0;

QY 241 ATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATT 300
DB |||||
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DB |||||
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DB |||||
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DB |||||
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wittig,R., Poustka,A., Mollenhauer,J. and Schadendorf,D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 6 06-MAY-2004;
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(DE)
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RESULT 5
LOCUS HUMHSEM 2530 bp mRNA linear PRI 08-MAY-1995
DEFINITION Homo sapiens semaphorin-III (Hsma-III) mRNA, complete cds.
ACCESSION L26081
VERSION L26081.1 GI:799328

semaphorin.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 2530)
Kolodkin,A.L., Mathes,D.J. and Goodman,C.S.
The semaphorin genes encode a family of transmembrane and secreted
growth cone guidance molecules
Cell 75 (7), 1389-1399 (1993)
94094332
8269517
On May 8, 1995 this sequence version replaced gi:436559.
Original source text: Homo sapiens (human).
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G31703
LOCUS SW581973 Eric D. Green Homo sapiens STS genomic, sequence tagged
site.
ACCESSION G31703
VERSION G31703.1 GI:1916428
KEYWORDS STS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2530)
Bouffard, G.G., Iyer, L.M., Idol, J.R., Braden, V.V., Cunningham, A.F.,
Weintraub, L.A., Mohr-Tidwell, R.M., Peluso, D.C., Fulton, R.S.,
Leckie, M.P., and Green, E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
97189344
9037602
2 (bases 1 to 2530)
Green, E.D.
Human chromosome 7 STSs (1997)
Unpublished (1997)
Synonyms: SEMIII
GDB_DSEG: SEMIII
Contact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Bethesda, MD 20892
Tel: 3014020201
Fax: 3014024735
Email: egreen@nhgri.nih.gov
Primer A: CCTGGAAGTCATTGCACAG
Primer B: GGTATGCTGCGCTTTGCCG
STS size: 230
PCR Profile:
Presoak: 0 degrees C for 0.00 minute(s)
Denaturation: 92 degrees C for 0.17 minute(s)
Annealing: 55 degrees C for 1.00 minute(s)
Polymerization: 72 degrees C for 1.00 minute(s)
PCR Cycles: 35
Thermal Cycler: PerkinElmer 9600
Protocol:
Template: 30-100 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
Buffer:
MgCl2: 1.5 mM
KCl: 100 mM
Tris-HCl: 10 mM
NH4Cl: 5 mM
pH: 8.6
This STS has been incorporated into the NHGRI chromosome 7
physical map, but was developed by another investigator. See
GenBank record: U26081 For additional information about the NHGRI
chromosome 7 mapping project, see
http://www.nhgri.nih.gov/DIR/GRB/CHR7. Also see Genomics
11:548-64 (1991) [MUID=92128937].
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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ACCESSION	AR040598					
VERSION	AR040598.1 GI:5959961					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 2601)					
AUTHORS	Goodman,C.S., Kolodkin,A.L., Matthes,D., Bentley,D.R. and O'Connor,T.					
TITLE	Semaphorin gene family					
JOURNAL	Patent: US 5807826-A 53 15-SEP-1998;					
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SOURCE Unknown.
ORGANISM Unknown.
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AUTHORS 1 (bases 1 to 2601)
Goodman,C.S., Kolodkin,A.L., Matthes,D., Bentley,D.R. and
O'Connor,T.
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JOURNAL Patent: US 5639856-A 53 17-JUN-1997;
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AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 2074 06-SEP-2002;
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JOURNAL Submitted (03-SEP-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LJNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LJNL at: <http://image.ljnl.gov>
Series: IRAK Plate: 125 Row: 0 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677910.

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ORIGIN

Query Match 75.7%; Score 2050; DB 10; Length 4013;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 2281; Conservative 0; Mismatches 295; Indels 14; Gaps 4;
QY 118 TTTCAGAGTTGTTGAACCTCTCGGCCGACAAATACAGGAAGAGACTAAAGCAGCAA 177
DB 215 TTTCAGAGTTGTTGAACCTCTCGGCCGACAAATACAGGAAGAGCTCGCCAGCTC 274
QY 178 AGGACCTACAGCGTCTGAGCATAGGGCTGGTAACTAGAGTTGTCTTCTTCTGGGG 237
DB 275 AGGACCTCAGCGTCTGAGCATAGGGCTGGTAACTAGAGTTGTCTTCTTCTGGGG 334

QY 238 AGTATTACTTACAGCAAGCAGCAAACTATCAGAAATGGGAAGAAACAATGTCCCAAGGCTGAA 297
DB 335 TGTATTACTTACAGCCAGCAGCAAACTATGCAAAACGGAAGAAACAATGTCCCAAGCTGAA 394
QY 298 ATTATCCTTACAAAGAAATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTGGCCAA 357
DB 395 ATTATCGTACAAAGAAATGTTGGAATCCAAACAATGTGATCACTTTTAATGGCTGGCCAA 454
QY 358 CAGCTCCAGTTATCATACCTTCTCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGC 417
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DB 515 AAAGATACATATATTTTCAATTCGACCTGTTTAATATCAAGGATTTTCAAAAGATTGTGTG 574
QY 478 GCCAGTATCTTACACAGAGAGATGATGCAAGTGGCTGGGAAGAGACATCTCGAAAGA 537
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DB 635 ATGTGCCAATTTTCAACAGGTCTCTGGAGGCTTATATCAGACTCACTTGTATGCCTGTGG 694
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DB 1235 ATGAACTCTAAAGATCTTAAATAATCCGATCGTCTATGAGTGTTCACAAACATCAAGCAA 1294
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 QY 1975 CATATTTTGGAAATGAGTCCGAAGTCCGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 2034
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 ACCESSION D85028.2 GI:18389545
 VERSION collapse-1.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Taniguchi, M., Yuasa, S., Fujisawa, H., Naruse, I., Saga, S., Mishina, M.
 and Yagi, T.
 Disruption of semaphorin III/D gene causes severe abnormality in
 peripheral nerve projection
 Neuron 19 (3), 519-530 (1997)
 97470885
 9331345
 REFERENCE 2 (bases 1 to 5952)
 Taniguchi, M.
 Direct Submission
 Submitted (02-MAY-1996) Masahiko Taniguchi, Department of
 Biochemistry and Molecular Biology, Graduate School of Medicine,
 The University of Tokyo, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033,
 Japan (E-mail: taniguchi@m.u-tokyo.ac.jp, Tel: 81-3-5802-2925,
 Fax: 81-3-3813-8732)
 On Jan 28, 2002 this sequence version replaced gi:1313903.
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ORIGIN

Query Match 75.7%; Score 2050; DB 10; Length 5952;

Best Local Similarity 88.1%; Pred. No. 0;

Matches 2281; Conservative 0; Mismatches 295; Indels 14; Gaps 4;

QY	118	TTTCCAGATGTTTGAACCTCTCTGCGCCGACAAATACAGGAAGGAGACATAAGCAGCAA	177
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QY	178	AGGGACCTACAGCGCTCTGAGCATGGCGTGGTTAACTAGGATGTCGTCTTTCTGGGG	237
DB	630	AGGGACCTCAGCGCTCTGAGCATGGCGTGGTTCACTGGGATGGCTGTCTTTCTGGGG	689
QY	238	AGTATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGAAACAATGTCCCAAGGCTGAA	297
DB	690	TGTATTACTTACAGCCAGAGCAAACTATGCAAAACGGAAAGAAACAATGTGCCAAGACTGAA	749
QY	298	ATTATCTCAAGAANAATGTTGGAATCCAACTATGATGATCACTTCAATGGCTTGGCCAA	357
DB	750	ATTATCGTACAAAGAAATGTTGGAATCCAACTATGATGATCACTTTTAATGGCTTGGCCAA	809
QY	358	CAGCTCCAGTATCATACCTCTCTTTGGATGAGGAACGGAGTAGGCTGATGTTGGAGC	417
DB	810	CAGCTCCAGTATCCACACCTTCTCTGGATGAAGAACGGAGTAGACTATATGTTGGAGC	869
QY	418	AAAGGATCAATATTTTCAATCGACCTGGTGTAAATATCAAGGATTTTCAAAAGATTTGTG	477
DB	870	AAAAGATCATATATTTTCAATCGACTTGTGAACATTAAGATTTTCAAAAGATTTGTG	929
QY	478	GCGAGTATCTACACAGAGAGATGAATGCAAGTGGGCTGGAAGAAGACATCCTGAAGA	537
DB	930	GCGAGTATCTTACAGAGAGAGATGAATGCAAAATGGGCTGGAAGAAGATATCTGAAAGA	989
QY	538	ATGTGCTAATTTTCACTCAAGTACTTAAGGCATATATCACTGCTGAGCTGAGCCCTGGG	597
DB	990	ATGTGCCAATTTTCACTCAAGTCTTGAGGCTTATATCACTGCTGAGCTGAGCTGAG	1049
QY	598	AACGGGGCTTTTCACTCAATTTGCACTTACATTTGAAATTTGACATCATCTCTGAGGACAA	657
DB	1050	NACTGGGGCTTTTCCATCCATCTGCACCTATATGAGTTGACATCATCTCTGAGGACAA	1109
QY	658	TATTTTAAAGCTGGAGAACTCAATTTTGAAGAACCGCCCTGGGAAGAGTCCATATGACCC	717
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QY	718	TAAGCTGCTGACAGCATCCTTTTAAATAGATGGAAATTTATCTCTGGAACCTGACCTGA	777
DB	1170	CAAACTACTGACTGCTCTCTTAAATAGCGGTGAGTTGTACTCTGGAACCTGCTGCGGA	1229
QY	778	TTTTTATGGGGGAGACTTTTGTCTATCTTCCGAACTCTTGGGCACCCACCCCAATCAGGAC	837
DB	1230	CTTCATGGGACGGGACTTCGCTATCTTCAAGACACTGCGGGCACCATCACCCTCATCAGAC	1289
QY	838	AGAGCAGCATGATTTCCAGTGGCTCAATGATCAAAAGTTTCATATGAGTGGCCCACTCATCTC	897
DB	1290	GGAGCAGCATGACTCCCGGTGGCTCAATGATCTAGATTCATCAGTGGCCCATCTCATCC	1349
QY	898	AGAGAGTGAATCTCTGAGATGACAAAGTATATCTTTTCTTCGTTGAAATGGCAATAGA	957
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QY	958	TGAGAACTCTTGGAAAAGCTTACTCACGCTAGATAGGTGAGATATGCAAGATGACTTT	1017
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QY	1198	CATTTTCAAGGATCAGCGCTGTGTATGTATAGCATGAGTGTATGAGAGGGTGTCTCT	1257
DB	1650	CATCTTTTAAAGGATCTGTGTGTGATGATACAGCATGAGTGTATGAGAGGGTGTCTCT	1709
QY	1258	TGTTCCATATGCCCCCAGGAGTGGACCAACTATCAATGGGTGCCTTATCAAGGAAGAGT	1317
DB	1710	TGTTCCATATGCTCACAGAGATGGTCCCAACTATCAGTGGGTGCCTTACCAAGGAAGAGT	1769
QY	1318	CCCCATATCCAGCGCCAGGAACCTTGTCCAGCAAAAACATTTGGTGGTGTGTGACTCTACAAA	1377
DB	1770	CCCTTATCCAGCGCCAGGAACCTTGTCCAGTAAAAACATTTGGCGGATTTGACTCCACAAA	1829
QY	1378	GGACCTTCTGTATGATTTATAACCTTTCRAAGAGTCACTCCAGCCATCTACAATCCAGT	1437
DB	1830	GGACCTTCTGTATGATGATTAACCTTTTGCAGGAAGTCACTCCAGCCATCTACAATCCAGT	1889
QY	1438	GTTCCTCTATGAACAATCGCCCAATAGTATCAAAACGGATGTAAATTTATCAATTTACACA	1497
DB	1890	GTTCCTCTATTAATATCGCCCGATCATGATCAAAACAGATGTAAATTTATCAGTTACACA	1949
QY	1498	AATTTCTGTAGCCAGTGGATGCAAGAGATGACAGTATGATGTTTATGTTTATCGGAAC	1557
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QY	1618	AGAGGTTCTGCTGGGAAGAAATGACAGTTTTTCGGGAACCGACTGCTTATTTTTCAGCAATGGA	1677
DB	2070	AGAGGTTCTTCTGGGAAGAAATGACCGCTTTCGGGAACCGACTGCTTATTTTTCAGCAATGGA	2129
QY	1678	GCTTTTCACTAAGCAGCAACAACTATATATGTTTCAACGGCTGGGGTGTGCCAGTCCC	1737
DB	2130	GCTTTTCACTAAGCAGCAACAGCTGTACATTTGGCTCAACTGCGGAGTGGCAAGCTTCC	2189
QY	1738	TTTACACCGGTGTATTTTACGGGAAGCGTGTGCTGAGTGTGTGCTCGCGGAGACCC	1797
DB	2190	TTTACACCGGTGTGATCTTATGGCAAGCGCTGTGCAAGTGTGCTCGCTCGGAGCCC	2249
QY	1798	TTTACTGTCTTGGGATGTTCTGCAATGTTCTCGCTATTTTCCACTTGCAGAGAGACGAC	1857
DB	2250	TTTACTGTCTTGGGATGTTGTTCTGCTCATGCTCATGCTACGCTATTTTCTGCAAGAGGCGAC	2309
QY	1858	AAGCAGCAAGATATAAAGAAATGGAGACCCACTGACTCTCACTGTTTTCAGACTT---	1914
DB	2310	AAGCAGCAAGATATAAAGAAATGGAGACCCACTGACTCTCACTGCTCTGACTTGCAGC	2369
QY	1915	TGATTAATCACCATGCGCCACAGCCCTGAAGAGAGATCATCTATGTTGTATAGAAATAGTAG	1974
DB	2370	TGATTAATCATCATGCGCCAGCCCTTGAAGAGAGAAATCATCTATGAGTGTGAAAGACAGTAG	2429
QY	1975	CACATTTTGGAAATCAGTCCGAACTGCGAGAGCGCTGTGCTTATTTGCAATTTCCAGAG	2034
DB	2430	TACATTTTGGAAATCAGTCCGAACTGCGAGAGCGCTTGGTATATTTGCAATTTCCAGAG	2489
QY	2035	GCGAAATGAAGCGCAAGAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCA	2094
DB	2490	GAGAATGAAGATCGAAAGAGGAGATCAGATGGGTGATCATATCATCAGGACAGCAACA	2549
QY	2095	AGGCTTCTGCTACCTGATCTTACACAGAGATTCAGGCAATTTACCTCTGCAATCGCGT	2154

ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 Giger, R.I.
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2319)
 Giger, R.I.
 JOURNAL Direct Submission
 TITLE Submitted (22-JAN-1996) R.I. Giger, Netherlands Inst. for Brain
 Research, Meibergdreef 33, 1105 AZ, Amsterdam, NETHERLANDS
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ORIGIN

Query Match 70.5%; Score 1909.4; DB 10; Length 2319;
 Best Local Similarity 89.3%; Pred. No. 0;
 Matches 2070; Conservative 0; Mismatches 246; Indels 3; Gaps 1;

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VERSION U02528.1 GI:410078
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SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
AUTHORS Luo, Y., Raible, D. and Raper, J. A.
TITLE Collapsin: a protein in brain that induces the collapse and
paralysis of neuronal growth cones
JOURNAL Cell 75 (2), 217-227 (1993)
MEDLINE 94006554
PUBMED 8402908
REFERENCE
AUTHORS Luo, Y.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1993) Yuling Luo, Department of Neuroscience,
University of Pennsylvania, School of Medicine, Philadelphia, PA
19104 USA
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 01:06:12 ; Search time 1465 Seconds
(without alignments)
10946.470 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2517	92.9	2848	10	Ade25679 Human cDN
3	2508.4	92.6	2530	2	Aax75767 Human sem
4	2508.4	92.6	2530	6	Abs76512 cDNA enco
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7	2508.4	92.6	2530	12	Adq19750 Human sof
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12	718.6	26.5	3871	3	Aax37109 Human PRO
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ALIGNMENTS

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AC AAH47049;
XX
DT 29-OCT-2001 (first entry)
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KW Drug resistance; resistance gene; semaphorin D; B94; mel-14 antigen;
KW 24p3; proliferin; maspin; cancer; cytostatic; gene therapy; ss.
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PN WO200155455-A2.
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PD 02-AUG-2001.
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PF 31-JAN-2001; 2001WO-US003161.
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PR 31-JAN-2000; 2000US-0179191P.
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PA (MILL-) MILLENNIUM PHARM INC.
XX
PI (JINS/) JIN S.
XX
Jin S;
XX
WPI; 2001-488799/53.
XX
Determining if a compound modulates the drug resistance of a cell,
comprises determining the expression or activity level of a resistance
sequence in a cell in the presence of the test compound.
XX
Example 1; Fig 1A-B; 79pp; English.

The invention relates to a method of determining whether a test compound modulates the drug resistance of a cell that comprises determining the expression or activity level of resistance genes (e.g. semaphorin D, B94, mel-14 antigen, 24p3, proliferin or maspin) in a cell in the presence of the test compound, and comparing its expression or activity level in a cell without the test compound. The drug resistant sequences are useful in identifying drug resistant cells, in screening methods directed to the

CC identification of compounds that can modulate the drug resistance of a
 CC cell type or multiple cell types. An isolated resistance protein can be
 CC used as an immunogen to generate antibodies that bind the resistance
 CC protein. Resistance nucleic acids may be inserted into vectors and used
 CC as gene therapy vectors. An anti-resistance protein antibody may be used
 CC to isolate a resistance protein, or facilitate the purification of
 CC natural resistance protein from cells and of recombinantly produced
 CC resistance protein expressed in host cells. The methods are useful for
 CC treating a subject having a disorder, such as a drug-resistance cancer,
 CC characterized by aberrant resistance sequence expression or activity by
 CC administering to the subject a resistance modulator. The present sequence
 CC represents a semaphorin cDNA sequence, whose expression was increased in
 CC drug resistant EMT6 tumours
 XX
 SQ Sequence 2709 BP; 831 A; 560 C; 620 G; 698 T; 0 U; 0 Other;

Query Match 100.0%; Score 2709; DB 4; Length 2709;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2709; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTTATCGATGTTTAAACAAGCTTAGTAAATCGATGCCAGCTCGAGGGGTGTCG 60
 DB 1 AATCTTTTATTTTATCGATGTTTAAACAAGCTTAGTAAATCGATGCCAGCTCGAGGGGTGTCG 60

QY 61 ACCCAGCGCTCGGGAGTAGTGTGAGCTCGCCTGTTCTCCCAATGTGACCCAGTCTATTT 120
 DB 61 ACCCAGCGCTCGGGAGTAGTGTGAGCTCGCCTGTTCTCCCAATGTGACCCAGTCTATTT 120

QY 121 CCAGATTGTTGAATCTCTGGCGGCACAAATACAGGAAGGAAGTAAAGCAGCAAGG 180
 DB 121 CCAGATTGTTGAATCTCTGGCGGCACAAATACAGGAAGGAAGTAAAGCAGCAAGG 180

QY 181 GACCTACAGCGTCTGAGCATGGCTGGTGTAACTAGGATGTCCTCTTTCTGGGGAGT 240
 DB 181 GACCTACAGCGTCTGAGCATGGCTGGTGTAACTAGGATGTCCTCTTTCTGGGGAGT 240

QY 241 ATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGCAATGTGCCAAGGCTGAAAT 300
 DB 241 ATTACTTACAGCAAGAGCAAACTATCAGAAATGGGAAGCAATGTGCCAAGGCTGAAAT 300

QY 301 ATCTTACAAAGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAG 360
 DB 301 ATCTTACAAAGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAG 360

QY 361 CTCAGATTATCATCTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAA 420
 DB 361 CTCAGATTATCATCTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAA 420

QY 421 GGATCACATATTTTCAATCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGGCC 480
 DB 421 GGATCACATATTTTCAATCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGGCC 480

QY 481 AGTATCTTACACAGAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCGAAGAAATG 540
 DB 481 AGTATCTTACACAGAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCGAAGAAATG 540

QY 541 TGCTAATTTTCACTCAAGGTACTTAAAGCATATATCAGACTCTTGTAGCCTGTGGAA 600
 DB 541 TGCTAATTTTCACTCAAGGTACTTAAAGCATATATCAGACTCTTGTAGCCTGTGGAA 600

QY 601 GGGGCTTTTTCATCAATTTGCACTTAAAGGATGGAATATCTCTGAACTGAGGCAATAT 660
 DB 601 GGGGCTTTTTCATCAATTTGCACTTAAAGGATGGAATATCTCTGAACTGAGGCAATAT 660

QY 661 TTTTAAAGCTGGAGACTCACATTTTGAACCGGCGTGGGAGAGTCCATATGACCTTAA 720
 DB 661 TTTTAAAGCTGGAGACTCACATTTTGAACCGGCGTGGGAGAGTCCATATGACCTTAA 720

QY 721 GCTGCTGACAGCATCCCTTTTAAATAGATGGAAATTTATCTCTGAACTGAGGCTGATTT 780
 DB 721 GCTGCTGACAGCATCCCTTTTAAATAGATGGAAATTTATCTCTGAACTGAGGCTGATTT 780

QY 781 TATGGGCGAGACTTTGCTATCTTCGGAATCTTTGGGCAACCAACCAATCAGGACAGA 840

DB 781 TATGGGCGAGACTTTTGTCTTCCGAATCTTTGGGCAACCAACCAATCAGGACAGA 840

QY 841 GCAGCATGATTTCCAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGA 900

DB 841 GCAGCATGATTTCCAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGA 900

QY 901 GAGTGACAAATCTCGAAGATGACAAAGTATATCTTTTCTTCGTTGAAATGCAATAGATGG 960

DB 901 GAGTGACAAATCTCGAAGATGACAAAGTATATCTTTTCTTCGTTGAAATGCAATAGATGG 960

QY 961 AGAACACTCTCTGAAAAGCTACTCAGCTAGATAGGTGAGATATCAAGAAATGACTTTGG 1020

DB 961 AGAACACTCTCTGAAAAGCTACTCAGCTAGATAGGTGAGATATCAAGAAATGACTTTGG 1020

QY 1021 AGGGCAGAGAGTCTGGTGAATTAATGACAAACATCTCTCAAGCTCGTGTGATTTGCTC 1080

DB 1021 AGGGCAGAGAGTCTGGTGAATTAATGACAAACATCTCTCAAGCTCGTGTGATTTGCTC 1080

QY 1081 AGTGCCAGGTCCAAATGCGATTGACACATCTTTTGTGATGAATGCAAGGATGATTCCTAAT 1140

DB 1081 AGTGCCAGGTCCAAATGCGATTGACACATCTTTTGTGATGAATGCAAGGATGATTCCTAAT 1140

QY 1141 GAACCTTTAAAGATCCCTAAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCCAGTAACAT 1200

DB 1141 GAACCTTTAAAGATCCCTAAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCCAGTAACAT 1200

QY 1201 TTTCAAGGGATCAGCCGTGTGTATGATAGCATGATGATGAGAAAGGTTGCTCTTGG 1260

DB 1201 TTTCAAGGGATCAGCCGTGTGTATGATAGCATGATGATGAGAAAGGTTGCTCTTGG 1260

QY 1261 TCCATATGCCACAGGGATGCAACCACTATCAATGGTGGCTTATCAAGGAAGAGTCCC 1320

DB 1261 TCCATATGCCACAGGGATGCAACCACTATCAATGGTGGCTTATCAAGGAAGAGTCCC 1320

QY 1321 CTATCCAGCGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTGTGACTCTACAAAGGA 1380

DB 1321 CTATCCAGCGCCAGGAACTTGTCCAGCAAAACATTTGGTGGTTGTGACTCTACAAAGGA 1380

QY 1381 CTTTCTGATGATGTTTAACTTTTGAAGAGTCAATCCAGCCATGTACAAATCCAGTGT 1440

DB 1381 CTTTCTGATGATGTTTAACTTTTGAAGAGTCAATCCAGCCATGTACAAATCCAGTGT 1440

QY 1441 TCCTATGAACAAATCGCCCAATAGTATGATCAAAACCGATGATAATTAACAATAAT 1500

DB 1441 TCCTATGAACAAATCGCCCAATAGTATGATCAAAACCGATGATAATTAACAATAAT 1500

QY 1501 TGTCTGAGACCGAGTGGATGCAAGATGGAAGATGGAAGATGATGTTATTCGGAACAGA 1560

DB 1501 TGTCTGAGACCGAGTGGATGCAAGATGGAAGATGGAAGATGATGTTATTCGGAACAGA 1560

QY 1561 TGTGGGACCGTCTTAAAGTATGTTTCAATTTCTTAAGGAGCTTGGTATGATTTAGAGA 1620

DB 1561 TGTGGGACCGTCTTAAAGTATGTTTCAATTTCTTAAGGAGCTTGGTATGATTTAGAGA 1620

QY 1621 GGTCTGCTGGAAGAAATGACAGTTTTTTCGGAACCGACTCTATTTTCAGCAATGGAGCT 1680

DB 1621 GGTCTGCTGGAAGAAATGACAGTTTTTTCGGAACCGACTCTATTTTCAGCAATGGAGCT 1680

QY 1681 TTCCAATAAGCAGCAACAACTATATATATGTTTCAACGGCTGGGTTGCCAGCTCCCTTT 1740

DB 1681 TTCCAATAAGCAGCAACAACTATATATATGTTTCAACGGCTGGGTTGCCAGCTCCCTTT 1740

QY 1741 ACACCGTGTGATATTTACGGGAAGGCTGCTGAGTGTGCTCGCCCGGAGACCTTTA 1800

DB 1741 ACACCGTGTGATATTTACGGGAAGGCTGCTGAGTGTGCTCGCCCGGAGACCTTTA 1800

QY 1801 CTGTCTGGGATGCTTCTGATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAG 1860

DB 1801 CTGTCTGGGATGCTTCTGATGTTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAG 1860

QY 1861 ACGACAGATATAGAAATGGAGACCACTGACTCACTGTTTACACTTACACCATGATAA 1920


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Db 1861 ACGACAAGATATAAGAAATGGAGACCCACTGACTCTACTCTTTCAGACTTACACCATGATAA 1920
Qy 1921 TCACCATGCCCACAGCCCTGGAAGAGAGAAATCATCTATGTGTAGAGAAATAGTAGCACATT 1980
Db 1921 TCACCATGCCCACAGCCCTGGAAGAGAGAAATCATCTATGTGTAGAGAAATAGTAGCACATT 1980
Qy 1981 TTTGGAAATCGAGTCCGAAGTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGGCGGAA 2040
Db 1981 TTTGGAAATCGAGTCCGAAGTCCGAGAGAGCGTGGTCTATTGGCAATTCAGAGGCGGAA 2040
Qy 2041 TGAAGAGCGAAAAGAGAGATCAGAGTGGATGATCATATCATCATCAGGACAGATCAAGGCCT 2100
Db 2041 TGAAGAGCGAAAAGAGAGATCAGAGTGGATGATCATATCATCATCAGGACAGATCAAGGCCT 2100
Qy 2101 TCTGCTACGTAGTCTTACAACAGAGGATTTCAGGCAATTAACCTCTGCGATGCGGTGGAACA 2160
Db 2101 TCTGCTACGTAGTCTTACAACAGAGGATTTCAGGCAATTAACCTCTGCGATGCGGTGGAACA 2160
Qy 2161 TGGGTTTCATACAACTCTTTTAAGGTAACTTGAAGTAACTTGAAGTAACTTGAAGTAACTTGA 2220
Db 2161 TGGGTTTCATACAACTCTTTTAAGGTAACTTGAAGTAACTTGAAGTAACTTGAAGTAACTTGA 2220
Qy 2221 AGAAGCTTCTTCTAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAG 2280
Db 2221 AGAAGCTTCTTCTAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAG 2280
Qy 2281 CATGACACCTAGCCAGAGGCTCTGGTACAGAGACTTTCAGGCTCATCAACCCACCCAA 2340
Db 2281 CATGACACCTAGCCAGAGGCTCTGGTACAGAGACTTTCAGGCTCATCAACCCACCCAA 2340
Qy 2341 TCTCAACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
Db 2341 TCTCAACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400
Qy 2401 GCAAGGCGCAGACATACCCAGGGAACAGTAACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2460
Db 2401 GCAAGGCGCAGACATACCCAGGGAACAGTAACTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2460
Qy 2461 GAAAGGTAGAAACAGAGGACCCACCAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGC 2520
Db 2461 GAAAGGTAGAAACAGAGGACCCACCAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGC 2520
Qy 2521 ATTACTCTAGAAACCTCAACAGATGAGAACTTGCTCTAGACAAATACCTGGAACAAACAA 2580
Db 2521 ATTACTCTAGAAACCTCAACAGATGAGAACTTGCTCTAGACAAATACCTGGAACAAACAA 2580
Qy 2581 TGCATATACATGAACTTTTTCATGCGCATTTATGATGATGATGATGATGATGATGATGATGATG 2640
Db 2581 TGCATATACATGAACTTTTTCATGCGCATTTATGATGATGATGATGATGATGATGATGATGATG 2640
Qy 2641 AGCTGAGTTCCACCAATTATAAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTTT 2700
Db 2641 AGCTGAGTTCCACCAATTATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2700
Qy 2701 CCTAATACC 2709
Db 2701 CCTAATACC 2709
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RESULT 2

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ADE25679
ID ADE25679 standard; cDNA; 2848 BP.
XX
AC ADE25679;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human cDNA differentially expressed in foam cells #83.
XX
KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
XX cardiovascular disease; atherosclerosis.
OS Homo sapiens.
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XX US2003194721-A1.
PN 16-OCT-2003.
XX
PP 18-SEP-2002; 2002US-00247671.
XX
PR 19-SEP-2001; 2001US-0323784P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX WPI; 2003-875398/81.
DR P-PSDB; ADE25760.
XX
PT Combination containing several polynucleotide that are differentially
PT expressed in foam cells and complements of the polynucleotides, useful
PT for diagnosing cardiovascular disease or atherosclerosis.
XX
PS Claim 1; SEQ ID NO 83; 37pp; English.
XX
CC The invention relates to a combination comprising several polynucleotides
CC having any one of 127 sequences (S1) such as the sequence of human
CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
CC hydrolase, human GGI-142 protein mRNA, human K+ channel beat 2 subunit
CC mRNA, etc., and their complements. The cDNAs are differentially expressed
CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
CC sequences, an expression vector containing the nucleic acids, a host cell
CC containing the vector, a purified polypeptide appearing as ADE25750 and
CC ADE25751, producing a protein by culturing the host cell, and a
CC composition comprising a purified antibody that specifically binds to the
CC proteins. The foam cell-expressed nucleic acids are useful for a high
CC throughput detection of differential expression of one or more
CC polynucleotides in a sample. The sample is from a subject with
CC atherosclerosis and comparison with a standard defines early, mid or late
CC stages of the disorder. The foam cell-expressed nucleic acids are useful
CC for high throughput screening of a library of molecules or compounds to
CC identify a ligand which binds a polynucleotide. The library is chosen
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
CC useful for a high throughput screening of library of molecules or
CC compounds to identify at least one ligand which specifically binds a
CC protein, for purifying a ligand from a sample for making an antibody. The
CC foam cell-expressed nucleic acids are useful for diagnosing
CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
CC as elements on a microarray which can be used for detecting related
CC polynucleotide in a sample, diagnosing cardiovascular disease,
CC atherosclerosis. The present sequence represents a cDNA whose expression
CC is upregulated in LPS treated foam cells.
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Sequence 2848 BP; 894 A; 569 C; 636 G; 749 T; 0 U; 0 Other;

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Query Match 92.9%; Score 2517; DB 10; Length 2848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 CTGCAGCATGGGCTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTGCAGCATGGGCTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 68

Qy 253 AAGAGCAAACTATCAGAATGGGAAGAACAAATGCGCAAGGCTGAAATTCCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAATGGGAAGAACAAATGCGCAAGGCTGAAATTCCTTACAAAGA 128

Qy 313 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCA 188

Qy 373 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATT 432
Db 189 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATT 248
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QY 433 TTCAATTCGACCTGGTTAATATCAAGGAAATTTCAAAAGATTGTGTGGCCAGTATCTTACAC 492
 Db 249 TTCAATTCGACCTGGTTAATATCAAGGAAATTTCAAAAGATTGTGTGGCCAGTATCTTACAC 308
 QY 493 CAGAGAGATGAATGCAAGTGGGCTGGGAAAGACATCTCTGAAAGAAATGTCTAAATTTCAAT 552
 Db 309 CAGAAAGATGAATGCAAGTGGGCTGGGAAAGACATCTCTGAAAGAAATGTCTAAATTTCAAT 368
 QY 553 CAAGGTACTTAAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAAGCGGGGCTTTTCA 612
 Db 369 CAAGGTACTTAAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAAGCGGGGCTTTTCA 428
 QY 613 TCCAAATTTGCACCTACATTTGAAATTTGGAATCATCTCTGAGGACAAATATTTTAAAGCTGGA 672
 Db 429 TCCAAATTTGCACCTACATTTGAAATTTGGAATCATCTCTGAGGACAAATATTTTAAAGCTGGA 488
 QY 673 GAACTCACAATTTTGAAGCGGCTGGGAAAGAGTCCATATGACCTTAAGCTCTGACAGC 732
 Db 489 GAACTCACAATTTTGAAGCGGCTGGGAAAGAGTCCATATGACCTTAAGCTCTGACAGC 548
 QY 733 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGAACTGCACTGATTTTATGGGCGAGA 792
 Db 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGAACTGCACTGATTTTATGGGCGAGA 608
 QY 793 CTTTGTCTATCTTCCGAACCTCTTTGGGCACCAACCAATCAGGACAGAGCAGCATGATTC 852
 Db 609 CTTTGTCTATCTTCCGAACCTCTTTGGGCACCAACCAATCAGGACAGAGCAGCATGATTC 668
 QY 853 CAGGTGGCTCAATGATCCAAAGTTTCTTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTTCTTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
 QY 913 TCAAGATGACAAAGTATACCTTTCTCGTCAAAATGCAATAGATGGAGAACACTCTGG 972
 Db 729 TCAAGATGACAAAGTATACCTTTCTCGTCAAAATGCAATAGATGGAGAACACTCTGG 788
 QY 973 AAAAGTACTCAGCTAGATAGGTGAGATGCAAGATGATCTTTGAGGGGCACAGAAG 1032
 Db 789 AAAAGTACTCAGCTAGATAGGTGAGATGCAAGATGATCTTTGAGGGGCACAGAAG 848
 QY 1033 TCTGGTGAATAATGGACAAACATTCCTCAAGCTGTCTGATTTGCTCAGTCCAGGTCC 1092
 Db 849 TCTGGTGAATAATGGACAAACATTCCTCAAGCTGTCTGATTTGCTCAGTCCAGGTCC 908
 QY 1093 AAATGGCATTTGACACTCATTTTGTGAACTGAGAGATGATTCCTAAATGAACTTTTAAAGA 1152
 Db 909 AAATGGCATTTGACACTCATTTTGTGAACTGAGAGATGATTCCTAAATGAACTTTTAAAGA 968
 QY 1153 TCCTAAAAATCCAGTTGTATATGGAGTGTGTTACGACTTCCAGTAAACATTTTCAAGGGATC 1212
 Db 969 TCCTAAAAATCCAGTTGTATATGGAGTGTGTTACGACTTCCAGTAAACATTTTCAAGGGATC 1028
 QY 1213 AGCCGTGTGTATGTATAGATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1272
 Db 1029 AGCCGTGTGTATGTATAGATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1088
 QY 1273 CAGGGATGACCCCAACTATCAATGGTGTCTTATCAAGGAAGTCCCTCATCCAGGGC 1332
 Db 1089 CAGGGATGACCCCAACTATCAATGGTGTCTTATCAAGGAAGTCCCTCATCCAGGGC 1148
 QY 1333 AGGAACTTGTCCAGCAAAACATTTGGTGGTTTGA CTCTCAAAAGGACCTTCTCTGATGA 1392
 Db 1149 AGGAACTTGTCCAGCAAAACATTTGGTGGTTTGA CTCTCAAAAGGACCTTCTCTGATGA 1208
 QY 1393 TGTATTAACCTTTGCAAGAGTCAATCCAGGCATGTACAACTCAGTGTCTCTATGACAA 1452
 Db 1209 TGTATTAACCTTTGCAAGAGTCAATCCAGGCATGTACAACTCAGTGTCTCTATGACAA 1268
 QY 1453 TCGCCCAATAGTGCATCAAAACCGATGTAATTTATCAATTTACAAAATTTGCTGTAGACCG 1512
 Db 1269 TCGCCCAATAGTGCATCAAAACCGATGTAATTTATCAATTTACAAAATTTGCTGTAGACCG 1328
 QY 1513 AGTGGATGCAGAAGATGGACAGTATGATGTTATGTTTATCGGAAACAGATGTTGGGACCGT 1572

Db 1329 AGTGGATGCAGAAGATGCACAGTATGATGTTATGTTTATCGGAAACAGATGTTGGACCGT 1388
 QY 1573 TCTTAAAGTAGTTTCAATTCCTTAAGGAGACTGGTATGATTTAGAAAGGTTCTCTCTGA 1632
 Db 1389 TCTTAAAGTAGTTTCAATTCCTTAAGGAGACTGGTATGATTTAGAAAGGTTCTCTCTGA 1448
 QY 1633 AGAAATGACAGTTTTCGGGAAACCACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1692
 Db 1449 AGAAATGACAGTTTTCGGGAAACCACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508
 QY 1693 GCACCAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTTCCCTTATACCCGGTGA 1752
 Db 1509 GCACCAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTTCCCTTATACCCGGTGA 1568
 QY 1753 TATTTACCGGAAAGCGTGTCTGAGTGTGCTCGCCGAGACCTTACTGTCTTGGGA 1812
 Db 1569 TATTTACCGGAAAGCGTGTCTGAGTGTGCTCGCCGAGACCTTACTGTCTTGGGA 1628
 QY 1813 TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAAAGAGAGCACAAGACGACAAGATAT 1872
 Db 1629 TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAAAGAGAGCACAAGACGACAAGATAT 1688
 QY 1873 AAGAAATGGAGACCCACTGACTCTGCTTTCAGACTTACCAATGATAATCACCATGGCCA 1932
 Db 1689 AAGAAATGGAGACCCACTGACTCTGCTTTCAGACTTACCAATGATAATCACCATGGCCA 1748
 QY 1933 CAGCCCTCAAGAGAGAAATCATCTGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1992
 Db 1749 CAGCCCTCAAGAGAGAAATCATCTGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1808
 QY 1993 TCCGAAGTCGACAGAGAGCGCTGCTATTTGGCAATTCAGAGGGCGAAATGAAGAGCGAAA 2052
 Db 1809 TCCGAAGTCGACAGAGAGCGCTGCTATTTGGCAATTCAGAGGGCGAAATGAAGAGCGAAA 1868
 QY 2053 AGAAGAGATCAGAGTGGAGTATCATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 2112
 Db 1869 AGAAGAGATCAGAGTGGAGTATCATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 1928
 QY 2113 TCTCAACACAGAGAGGATTCAGGCCAATTCCTCTGCCATCGGTGGAAACATGGGTTTCATACA 2172
 Db 1929 TCTCAACACAGAGAGGATTCAGGCCAATTCCTCTGCCATCGGTGGAAACATGGGTTTCATACA 1988
 QY 2173 AACTCTTCTTAAAGSTAAACCTCGGAAGTCAATGACACAGAGCATTTGGAGAACTTCTTCA 2232
 Db 1989 AACTCTTCTTAAAGSTAAACCTCGGAAGTCAATGACACAGAGCATTTGGAGAACTTCTTCA 2048
 QY 2233 TAAAGATGATGATGAGATGGCTTAAAGCCAAAGAAATGTCCAATAGCATGACACCTAG 2292
 Db 2049 TAAAGATGATGATGAGATGGCTTAAAGCCAAAGAAATGTCCAATAGCATGACACCTAG 2108
 QY 2293 CCAGAGGCTCTGTTACAGAGACTTTCATGCTCATCAACCCCAATCTCAACACGAT 2352
 Db 2109 CCAGAGGCTCTGTTACAGAGACTTTCATGCTCATCAACCCCAATCTCAACACGAT 2168
 QY 2353 GGATGAGTCTCTGAAACAAAGTTTGGAAAGGAGCCGAAAAACAACTCGGCAAGGCCAGG 2412
 Db 2169 GGATGAGTCTCTGAAACAAAGTTTGGAAAGGAGCCGAAAAACAACTCGGCAAGGCCAGG 2228
 QY 2413 ACATACCCCGAGGAAACAGTAAACAAATGGAGACCTTACAGAAATAGAAAGGTAGAAA 2472
 Db 2229 ACATACCCCGAGGAAACAGTAAACAAATGGAGACCTTACAGAAATAGAAAGGTAGAAA 2288
 QY 2473 CAGGAGGACCCAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCAATACCTCTACA 2532
 Db 2289 CAGGAGGACCCAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCAATACCTCTACA 2348
 QY 2533 AACCTCAAAACAGTAGTAAACCTTCCCTAGACAAATACTGAGAAAAACAAATGCAATATACAT 2592
 Db 2349 AACCTCAAAACAGTAGTAAACCTTCCCTAGACAAATACTGAGAAAAACAAATGCAATATACAT 2408
 QY 2593 GAACTTTTTCATGTCATTTGAGTGTGATGTTTACATGTTGGGAAATTCAGCTGAGTTCCA 2652

Db 2409 GAACTTTTTCATGTCATATGATGATGTTTACATGTTGGGAATTCAGCTGAGTTCA 2468
Qy 2653 CCAATTATAAATAATCCATGAGTAACCTTCTTAATAGGCTTTTTCCTTAATACC 2709
Db 2469 CCAATTATAAATAATCCATGAGTAACCTTCTTAATAGGCTTTTTCCTTAATACC 2525

RESULT 3
ID AAX75767 standard; DNA; 2530 BP.
XX AAX75767;
XX 22-JUL-1999 (first entry)
XX Human semaphorin III DNA.

Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
frameshift mutation; age-related disease; neurodegenerative disorder;
Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
Huntington's disease; multiple sclerosis; alcoholic liver disease;
diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
high mobility group protein-C; neuroendocrine specific protein A; ss.
Homo sapiens.
OS
XX
XX WO9845322-A2.
PN
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB000705.
XX
PR 10-APR-1997; 97US-0043163P.
XX
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX
XX WPI; 1998-609901/51.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
XX Disclosure; Fig 16; 258pp; English.

This invention describes a novel method for the diagnosis of a disease
caused by, or associated with, an RNA molecule that has a frameshift
mutation. The method is used to diagnose age-related diseases, especially
cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
and many others listed) or susceptibility to these disorders. The method
allows a definitive diagnosis of Alzheimer's disease in living patients,
at an early stage. It is based on the observation that disease may be
caused by mutations in RNA rather than DNA. The invention describes the
used of neuronal system RNA molecules, specifically proteins including
beta-amyloid precursor protein (beta-APP), the microtubule associated
proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence
encodes the wild type and mutant protein fragments represented in
AAY21264-Y21348

XX SQ Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;
Query Match 92.6%; Score 2508.4; DB 2; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 193 CTGCAGCATGGGCTGGTTAACTAGGATTTGTCCTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTGCAGCATGGGCTGGTTAACTAGGATTTGTCCTTTCTGGGAGTATTACTTACAGC 68
Qy 253 AAGAGCAAACTATCAGAAATGGGAAGCAAACTATGTCGCAAGGCTGAAATTTATCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGGAAGCAAACTATGTCGCAAGGCTGAAATTTATCTTACAAAGA 128
Qy 313 AATGTTGGAATCCAACTATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAACTATGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
Qy 373 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGATCACATATT 432
Db 189 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGATCACATATT 248
Qy 433 TTCATTGCACTGGTTTAAATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 492
Db 249 TTCATTGCACTGGTTTAAATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 308
Qy 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTCTAAATTTTCAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTCTAAATTTTCAT 368
Qy 553 CAAGGTACTTAAAGGCATATAATCAGACTCCTGAGGACATATTTTAAAGCTGGA 612
Db 369 CAAGGTACTTAAAGGCATATAATCAGACTCCTGAGGACATATTTTAAAGCTGGA 428
Qy 613 TCCAAATTTGCACTTACATTTGAAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 672
Db 429 TCCAAATTTGCACTTACATTTGAAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 488
Qy 673 GAACTCACAATTTTGAAGGCGGCTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 732
Db 489 GAACTCACAATTTTGAAGGCGGCTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 548
Qy 733 ATCCCTTTTAAATGAGAGATTAATCTCTGAACTGCAAGTGTATTTTATGGGCGAGA 792
Db 549 ATCCCTTTTAAATGAGAGATTAATCTCTGAACTGCAAGTGTATTTTATGGGCGAGA 608
Qy 793 CTTTGCTATCTCCGAATCTTTGGGCAACCAACCCCAATCAGGACAGCAGCATGATTC 852
Db 609 CTTTGCTATCTCCGAATCTTTGGGCAACCAACCCCAATCAGGACAGCAGCATGATTC 668
Qy 853 CAGGTGGGCTCAATGATCCAAAGTTTCATTTAGTCCCACTCTCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGGGCTCAATGATCCAAAGTTTCATTTAGTCCCACTCTCTCAGAGAGTGACAATCC 728
Qy 913 TGAAGATGACAAAGTATATCTTTTCTCGTGAAGTCAATAGATGGAAGAACACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTCGTGAAGTCAATAGATGGAAGAACACTCTGG 788
Qy 973 AAAAGCTACTCAGCTAGATAGTTCAGATATGCAAGATGACTTTGGAGGGGACAGAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGATAGTTCAGATATGCAAGATGACTTTGGAGGGGACAGAGAAG 848
Qy 1033 TCTGTGTAATAATGGCAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGCTCC 1092
Db 849 TCTGTGTAATAATGGCAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGCTCC 908
Qy 1093 AAATGGCATTTGACACTCAATTTTGTAGTGAATGCAGGATGTATTCTTAATGAACCTTTAAAGA 1152
Db 909 AAATGGCATTTGACACTCAATTTTGTAGTGAATGCAGGATGTATTCTTAATGAACCTTTAAAGA 968
Qy 1153 TCCTAAAAATCCAGTTGTATATGAGATGTTTACAGACTTCCAGTAAATTTTCAAGGATC 1212

969	Db	TCCTAAAAATCCAGCTTGATATGAGGATGTTTACGACTTCGAGTAAACATTTTCAAGGATC	1027
1213	Qy	AGCCGTGTGATGTATAGCATGAGTGCAGAGGGTGTCTCTTTGGTCCATATGCCCA	1272
1029	Db	AGCCGTGTGATGTATAGCATGAGTGCAGAGGGTGTCTCTTTGGTCCATATGCCCA	1088
1273	Qy	CAGGGATGGACCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGCC	1332
1089	Db	CAGGGATGGACCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGCC	1148
1333	Qy	AGGAACCTGTCCAGCAAAACATTTGGTGTGTTTGACTCTACAAAGGACCTTCTCATGA	1392
1149	Db	AGGAACCTGTCCAGCAAAACATTTGGTGTGTTTGACTCTACAAAGGACCTTCTCATGA	1208
1393	Qy	TGTTATAACCTTTGCCAAGAAGTCAATCAGGCATGTACAATCCAGTGTTCCTATGAACAA	1452
1209	Db	TGTTATAACCTTTGCCAAGAAGTCAATCAGGCATGTACAATCCAGTGTTCCTATGAACAA	1268
1453	Qy	TCGCCCAATAGTGAATCAAAACGGATGTAATATCAATTTACACAAATGTCTGACCG	1512
1269	Db	TCGCCCAATAGTGAATCAAAACGGATGTAATATCAATTTACACAAATGTCTGACCG	1328
1513	Qy	AGTGGATGCAGAGAATGCAAGTATGATGTATGTATTCGGAACAGATGTTGGGACCGT	1572
1329	Db	AGTGGATGCAGAGAATGCAAGTATGATGTATGTATTCGGAACAGATGTTGGGACCGT	1388
1573	Qy	TCCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTAGAGAGAGTCTGCTGGA	1632
1389	Db	TCCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTAGAGAGAGTCTGCTGGA	1448
1633	Qy	AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTAAGCA	1692
1449	Db	AGAAATGACAGTTTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTAAGCA	1508
1693	Qy	GCAACACTATATATTGGTTCAACGGCTGGGGTTGCCACGCTCCCTTTACACGGGTGTGA	1752
1509	Db	GCAACACTATATATTGGTTCAACGGCTGGGGTTGCCACGCTCCCTTTACACGGGTGTGA	1568
1753	Qy	TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGAGCCCTTACTGTGCTTGGGA	1812
1569	Db	TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGAGCCCTTACTGTGCTTGGGA	1628
1813	Qy	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGAGATAT	1872
1629	Db	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGAGATAT	1688
1873	Qy	AAGAAATGGAGACCCCACTGACTCTGTTTCAGACTTACACGATGATATCACCAATGGCCA	1932
1689	Db	AAGAAATGGAGACCCCACTGACTCTGTTTCAGACTTACACGATGATATCACCAATGGCCA	1748
1933	Qy	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGCACATTTTGGAAATCGAG	1992
1749	Db	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGCACATTTTGGAAATCGAG	1808
1993	Qy	TCCGAAGTCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGGCGAAATGAAGAGCGAAA	2052
1809	Db	TCCGAAGTCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGGCGAAATGAAGAGCGAAA	1868
2053	Qy	AGAAGAGATCAGATGGAGATGATCATATCATCAGAGACAGTCAAGGCCCTTCTGTTACGTAG	2112
1869	Db	AGAAGAGATCAGATGGAGATGATCATATCATCAGAGACAGTCAAGGCCCTTCTGTTACGTAG	1928
2113	Qy	TCTACACAGAGAGGTTTCAGGCAATTAACCTCTGCCATCGCGTGAAACATGGGTTCAVACA	2172
1929	Db	TCTACACAGAGAGGTTTCAGGCAATTAACCTCTGCCATCGCGTGAAACATGGGTTCAVACA	1988
2173	Qy	AACCTCTTCTAAGGTAAACCTTGGAAAGTCATTTCACACAGAGCATTTTGGAAAGAACTTCTTCA	2232
1989	Db	AACCTCTTCTAAGGTAAACCTTGGAAAGTCATTTCACACAGAGCATTTTGGAAAGAACTTCTTCA	2048
2233	Qy	TAAAGATGATGATGAGATGCTCTTAAGACCAAAAGAAATGTCCTAATAGCATGACACCTAG	2292
2049	Db	TAAAGATGATGATGAGATGCTCTTAAGACCAAAAGAAATGTCCTAATAGCATGACACCTAG	2108

Qy	2293	CCGAGAGGTC	TGGTACAGAGACT	TCATGAGCTC	ATCAACCA	CCCCCAAT	CTCAACAGAT	2352	
Db	2109	CCGAGAGGTC	TGGTACAGAGACT	TCATGAGCTC	ATCAACCA	CCCCCAAT	CTCAACAGAT	2168	
Qy	2353	GGATGAGTCT	GTGACAAAGCT	TTTGAAAGG	ACCGAGAC	CAAGAAAC	ACAGCTCGG	CAAAAGGCCAGG	2412
Db	2169	GGATGAGTCT	GTGACAAAGCT	TTTGAAAGG	ACCGAGAC	CAAGAAAC	ACAGCTCGG	CAAAAGGCCAGG	2228
Qy	2413	ACATACCCCA	GAGGAAACAGT	TAACAAAT	TGGAAGCA	CTTACAAGAA	AAAAAAGGAAGG	TAGAAA	2472
Db	2229	ACATACCCCA	GAGGAAACAGT	TAACAAAT	TGGAAGCA	CTTACAAGAA	AAAAAAGGAAGG	TAGAAA	2288
Qy	2473	CAGGAGGAC	CCACGAAT	TTTGAGAGG	GCACCCAGAG	GTGTCTGAG	CTGAGCTGC	ATTACCTCTAGA	2532
Db	2289	CAGGAGGAC	CCACGAAT	TTTGAGAGG	GCACCCAGAG	GTGTCTGAG	CTGAGCTGC	ATTACCTCTAGA	2348
Qy	2533	AACCTCAAA	CAAGTAGAA	ACTTGCCCTAG	ACAAATTA	CTGGAAAC	AAACAAAT	TGCAATATACAT	2592
Db	2349	AACCTCAAA	CAAGTAGAA	ACTTGCCCTAG	ACAAATTA	CTGGAAAC	AAACAAAT	TGCAATATACAT	2408
Qy	2593	GAACCTTTTT	TCATGGCA	TATATGTGGAT	GTGTTTCA	AAATGGTGGG	AAAAAT	TTCAGCTGAGTTCCA	2652
Db	2409	GAACCTTTTT	TCATGGCA	TATATGTGGAT	GTGTTTCA	AAATGGTGGG	AAAAAT	TTCAGCTGAGTTCCA	2468
Qy	2653	CCAATTAAAT	TAAATCCAT	GATGAAC	TTTTCCTAAT	TAGGCTTTTT	TTTTTC	2702	
Db	2469	CCAATTAAAT	TAAATCCAT	GATGAAC	TTTTCCTAAT	TAGGCTTTTT	TTTTTC	2518	

RESULT 4

ABS76512
ID ABS76512 standard: cDNA: 2530 BP.

AC ABS76512;

11-DEC-2002 (first entry)

DE CDNA encoding human ovarian cancer marker M473.

XX Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KW central nervous system disorder; bacterial meningitis; viral meningitis;
KW Alzheimer's disease; parkinson's disease; cerebral oedema; hydrocephalus
KW brain herniation; inflammation; encephalitis; testicular disorder;
KW nonbuccal granulomatous orchitis; connective tissue disorder;
KW heart disorder; ischemic heart disease; atherosclerosis; neoplasm;
KW histological type; carcinogenic; ovarian cancer marker; gene; ss.

XX Homo sapiens.

XX PN WO200271928-A2.

XX
19-SEP-2002

14-MAR-2002. 2002WO-IIS007826.

XX
PP 14-MAR-2001. 2001US-0276025P.

PR 14-MAR-2001; 2001US-0276026P.
 PP 10-AUG-2001; 2001US-0311732P.

PR 19-SEP-2001; 2001US-0323580P.
 PR 19-SEP-2001; 2001US-0323580P.
 PR 19-SEP-2001; 2001US-0323580P.

PR 26-SEP-2001; 2001US-0325102P.

XX

[illegible]

PI Meyers RE, Morrissey MP, Olafson

XX

DR P-PSDB; ABG96413.

3

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

Disclosure; Page 400; 481pp; English.

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the invention

Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB-6; Length 2530;

Best Local Similarity 100.0%; Pident. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PT	Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.
PT	
PT	
XX	
PS	Disclosure; Page 400; 481pp; English.
XX	
CC	The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. non-tuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the invention
CC	
XX	
SQ	Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;
Query Match	92.6%; Score 2508.4; DB-6; Length 2530;
Best Local Similarity	100.0%; Pident. No. 0;
Matches 2509;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	193 CTGACGATGGGCTGTTAACTAGGATGTCCTCTTTCTGGGGAGTATTCTTACAGC 252
DB	
QY	253 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCACAGGCTGAAATATCTCTACAAAGA 312
DB	
QY	69 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCACAGGCTGAAATATCTCTACAAAGA 128
DB	
QY	313 AATGTTGGAAATCCAAATGTCATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
DB	
QY	129 AATGTTGGAAATCCAAATGTCATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
DB	
QY	373 TACCTTCCCTTTGGATGAGAACGGAGTAGGCTGATGTTGGGCAAGATCACAATAT 432
DB	
QY	189 TACCTTCCCTTTGGATGAGAACGGAGTAGGCTGATGTTGGGCAAGATCACAATAT 248
DB	
QY	433 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTTGGCCAGATCTTTACAC 492
DB	
QY	249 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTTGGCCAGATCTTTACAC 308
DB	
QY	493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTTCTAAATTCAT 552
DB	
QY	309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTTCTAAATTCAT 368
DB	
QY	553 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAAACGGGGCTTTTCA 612
DB	
QY	369 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAAACGGGGCTTTTCA 428
DB	
QY	613 TCCAAATTTGACCTACATATGAAATGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 672
DB	
QY	429 TCCAAATTTGACCTACATATGAAATGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 488
DB	
QY	673 GAACTCACATTTTGAAGAACGGCGGTGGGAAGAGTCCATATGACCCCTTAAGCTGCTGACAGC 732

DB	489 GAACTCACATTTTGAAGAACGGCGGTGGGAAGAGTCCATATGACCCCTTAAGCTGCTGACAGC 548
QY	733 ATCCCTTTTAAATAGATGGAGAATATATCTCTGGAAGTCTGAGCTGATTTTATGGGGGAGGA 792
DB	549 ATCCCTTTTAAATAGATGGAGAATATATCTCTGGAAGTCTGAGCTGATTTTATGGGGGAGGA 608
QY	793 CTTTGTCTATCTTCCGAACTCTTTGGGGCAACCAACCAATCAGAGACAGAGCATGATTC 852
DB	609 CTTTGTCTATCTTCCGAACTCTTTGGGGCAACCAACCAATCAGAGACAGAGCATGATTC 668
QY	853 CAGGTGGCTCAATGATCCAAAGTTCATATAGTCCCACTCATCTCAGAGAGTGACAAATCC 912
DB	669 CAGGTGGCTCAATGATCCAAAGTTCATATAGTCCCACTCATCTCAGAGAGTGACAAATCC 728
QY	913 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCTGG 972
DB	729 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTCTGG 788
QY	973 AAAAGCTACTCAGCTAGGATAGGTCAGATATGCAAGATAGACTTTTGGAGGGCACAGAAG 1032
DB	789 AAAAGCTACTCAGCTAGGATAGGTCAGATATGCAAGATAGACTTTTGGAGGGCACAGAAG 848
QY	1033 TCTGTGTAATTAATGAGAACAACTTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCCTC 1092
DB	849 TCTGTGTAATTAATGAGAACAACTTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCCTC 908
QY	1093 AAATGGCATTTGACACTCATTTTGTGAACTGCAAGGATGATTTCTTAATGAACCTTTAAAGA 1152
DB	909 AAATGGCATTTGACACTCATTTTGTGAACTGCAAGGATGATTTCTTAATGAACCTTTAAAGA 968
QY	1153 TCCTAAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC 1212
DB	969 TCCTAAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC 1028
QY	1213 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCCA 1272
DB	1029 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCCA 1088
QY	1273 CAGGGATGAGCAACCACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTCTATCCAGGCC 1332
DB	1089 CAGGGATGAGCAACCACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTCTATCCAGGCC 1148
QY	1333 AGGAACCTTGTCCAGCAAAACATTTGGTGGTTTGTGCTCTCAAAAGGACCTTCTCTGATGA 1392
DB	1149 AGGAACCTTGTCCAGCAAAACATTTGGTGGTTTGTGCTCTCAAAAGGACCTTCTCTGATGA 1208
QY	1393 TGTATTAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGAAACAA 1452
DB	1209 TGTATTAACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGAAACAA 1268
QY	1453 TCGCCCAATAGTGTATCAAAACGGATGTAAATTTATCAATTTTACAAATTTGTCTAGACCG 1512
DB	1269 TCGCCCAATAGTGTATCAAAACGGATGTAAATTTATCAATTTTACAAATTTGTCTAGACCG 1328
QY	1513 AGTGGATGCAAGAGTGGACAGTATGTTTATGTTTATCGGAACAGATGTTGGGACCGT 1572
DB	1329 AGTGGATGCAAGAGTGGACAGTATGTTTATGTTTATCGGAACAGATGTTGGGACCGT 1388
QY	1573 TCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGAGTTCTGCTGGA 1632
DB	1389 TCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGAGTTCTGCTGGA 1448
QY	1633 AGAAATGACAGTCTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCA 1692
DB	1449 AGAAATGACAGTCTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508
QY	1693 GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA 1752
DB	1509 GCAACAACTATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGTGTGA 1568
QY	1753 TATTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTCTTGGGA 1812

Db 1569 TATTATCCGGAAGCGTGTGCTGAGTGTGCTGCCCGGAGACCCTTACTGTGCTGGGA 1628
Qy 1813 TGGTTCTGCTATGCTTCTGCTATTTTCCCACTCAAGAGACGACCAAGACGACAGATAT 1872
Db 1629 TGGTTCTGCTATGCTTCTGCTATTTTCCCACTCAAGAGACGACCAAGACGACAGATAT 1688
Qy 1873 AAGAAATGGAGACCCACTGACTCTGCTTGTGAGCTTTACACCATGATATACCATGGCCA 1932
Db 1689 AAGAAATGGAGACCCACTGACTCTGCTTGTGAGCTTTACACCATGATATACCATGGCCA 1748
Qy 1933 GAGCCTTGAAGAGAGATCATCTATGCTGTAGAGATAGTAGCACAATTTTGGATGCGAG 1992
Db 1749 GAGCCTTGAAGAGAGATCATCTATGCTGTAGAGATAGTAGCACAATTTTGGATGCGAG 1808
Qy 1993 TCCGAAGTCGACAGAGCGCTGCTTATTGGCAATTCAGAGCGCAATTAAGAGCGGAAA 2052
Db 1809 TCCGAAGTCGACAGAGCGCTGCTTATTGGCAATTCAGAGCGCAATTAAGAGCGGAAA 1868
Qy 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 1928
Qy 2113 TCTACAACAGAGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGTTCATACA 2172
Db 1929 TCTACAACAGAGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGTTCATACA 1988
Qy 2173 AACTCTTTTAAGTAAACCTCGAAGTCAATTCACACAGAGCAATTTGGAAAGCACTTCTTCA 2232
Db 1989 AACTCTTTTAAGTAAACCTCGAAGTCAATTCACACAGAGCAATTTGGAAAGCACTTCTTCA 2048
Qy 2233 TAAAGATGATGAGAGTGGCTTAAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGAGAGTGGCTTAAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
Qy 2293 CCAGAGGTCTGTCAGAGACTTCATGAGCTCTATCAACCAACCCCAATCTCAACAGAT 2352
Db 2109 CCAGAGGTCTGTCAGAGACTTCATGAGCTCTATCAACCAACCCCAATCTCAACAGAT 2168
Qy 2353 GATGAGTCTGTCAGAGACTTTGAAAAGGACCGCAAAACAACTGCGCAAGGCCAGG 2412
Db 2169 GATGAGTCTGTCAGAGACTTTGAAAAGGACCGCAAAACAACTGCGCAAGGCCAGG 2228
Qy 2413 ACATACCCCGAGGACAGTAAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGAGGACAGTAAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAA 2288
Qy 2473 CAGGAGGCCACGAAATTTGAGAGGCCACCGAGGAGTGTCTGAGCTGCATTAACCTCTAGA 2532
Db 2289 CAGGAGGCCACGAAATTTGAGAGGCCACCGAGGAGTGTCTGAGCTGCATTAACCTCTAGA 2348
Qy 2533 AACCTCAAAACAGTAGAAACTTGCCTAGACAATACTGGAAAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAAAACAGTAGAAACTTGCCTAGACAATACTGGAAAAACAAATGCAATATACAT 2408
Qy 2593 GAACCTTTTTCATGCGCAATATGAGATGTTTCAATGTTGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTCATGCGCAATATGAGATGTTTCAATGTTGGAAATTCAGCTGAGTTCCA 2468
Qy 2653 CCAATTATAAATAAATCCATGATTAACCTTCTTAATAGCTTTTTTTC 2702
Db 2469 CCAATTATAAATAAATCCATGATTAACCTTCTTAATAGCTTTTTTTC 2518

RESULT 5
ADD08933
ID ADD08933 standard; cDNA; 2530 BP.
XX
AC ADD08933;
XX
XX 01-JAN-2004 (first entry)
XX
DE Human semaphorin 3A encoding cDNA SEQ ID NO:9.
XX

KW screening; modulator; binding; neuropilin growth factor receptor;
KW vascular endothelial growth factor C;
KW vascular endothelial growth factor receptor 3; VEGF-C; VEGFR-3;
KW neuropilin; cytotostatic; nootropic; neuroprotective; vulnerary;
KW vasotrophic; cardiant; angiogenic process; nervous system growth;
KW nervous system function; cancer; ischaemia; cerebral infarction;
KW cerebral bleeding; Alzheimer's disease; myocardial infarction; human;
KW gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 16..2331
FT /*tag= a
FT /product= "semaphorin 3A"
XX
XX WO2003029814-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-EP011069.
XX
XX 01-OCT-2001; 2001US-0326326P.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX (LICN) LICENTIA LTD.
XX
XX Alitalo K, Karkkainen M, Karila K;
XX
XX WPI; 2003-381660/36.
XX P-PSDB; ADD08934.
XX
XX Screening for modulators of neuropilin and vascular endothelial growth
XX factor (VEGF)-C or VEGFR-3 interactions, comprises comparing interaction
XX of neuropilin and VEGF-C or VEGFR-3 in the presence and absence of a
XX modulator compound.
XX
XX Disclosure; SEQ ID NO 9; 181pp; English.
XX
XX The present invention describes a method of screening for modulators of
XX binding between a neuropilin growth factor receptor and a vascular
XX endothelial growth factor (VEGF)-C or VEGFR-3 polypeptide comprising
XX comparing the binding between neuropilin and VEGF-C or VEGFR-3 in the
XX presence and in the absence of a putative modulator compound. Also
XX described: (1) screening for selectivity of a modulator of VEGF-C, VEGFR-
XX 3 or neuropilin biological activity; (2) modulating growth, migration or
XX proliferation of cells in a mammalian organism; (3) a bispecific antibody
XX which specifically binds to a neuropilin receptor and a VEGF-C or VEGFR-3
XX polypeptide; (4) modulating neuronal growth or neuronal scarring in a VEGF
XX mammalian organism; and (5) a polypeptide comprising a fragment of a VEGF
XX -C that binds to a neuropilin receptor. The modulators have cytostatic,
XX nootropic, neuroprotective, vulnerary, vasotropic and cardiant
XX activities. The method is useful in modulating angiogenic processes and
XX nervous system growth and function, such as in the treatment of cancer,
XX wound, ischaemia, cerebral infarction/bleeding, Alzheimer's disease or
XX myocardial infarction. The polypeptide comprising a fragment of a VEGF-C
XX that binds to a neuropilin receptor, is useful for manufacturing a
XX medicament for the treatment of diseases characterised by aberrant
XX growth, migration or proliferation of cells that express a neuropilin
XX receptor. The present sequence encodes human semaphorin 3A, which is used
XX in the exemplification of the present invention.
XX
XX
SQ Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;
Query Match 92.6%; Score 2508.4; DB 10; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 193 CTGACGATGGCTGGTTAACTAGGATTTCTGCTTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTGACGATGGCTGGTTAACTAGGATTTCTGCTTTTCTGGGAGTATTACTTACAGC 68
Qy 253 AAGACAACTATCATCAGATGGGAACAACTGCGCAAGGCTGAATTTCTTACAAAGA 312

Db 69 AAGAGCAACTATCAGAAATGGGAGAAACAATGTGCCAAGGCTGAAATTAATCTTACAAGA 128
Qy
Db 313 AATGTGGAAATCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Qy
Db 129 AATGTGGAAATCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
Qy
Db 373 TACCTTCCCTTTTGGATGAGAAACGAGTAGGCTGTATGTTGAGCAAGGATCAATATT 432
Qy
Db 189 TACCTTCCCTTTTGGATGAGAAACGAGTAGGCTGTATGTTGAGCAAGGATCAATATT 248
Qy
Db 433 TTCAATTCGACCTGGTTTAAATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC 492
Qy
Db 249 TTCAATTCGACCTGGTTTAAATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC 308
Qy
Db 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAGAAATGTCTAAATTTCA 552
Qy
Db 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAGAAATGTCTAAATTTCA 368
Qy
Db 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCA 612
Qy
Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCA 428
Qy
Db 613 TCCAAATTCGACCTGATTTGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 672
Qy
Db 429 TCCAAATTCGACCTGATTTGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 488
Qy
Db 673 GAACTCACATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732
Qy
Db 489 GAACTCACATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548
Qy
Db 733 ATCCCTTTTAAATAGATGGAATTAATCTCTGAACTGCACTGATTTTATGGGGGAGA 792
Qy
Db 549 ATCCCTTTTAAATAGATGGAATTAATCTCTGAACTGCACTGATTTTATGGGGGAGA 608
Qy
Db 793 CTTTGTCTATCTTCGAACTCTTTGGGACACCAACCCCAATCAGGACAGACGATGATTC 852
Qy
Db 609 CTTTGTCTATCTTCGAACTCTTTGGGACACCAACCCCAATCAGGACAGACGATGATTC 668
Qy
Db 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCACCACTCATCTCAGAGAGTGACAATCC 912
Qy
Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCACCACTCATCTCAGAGAGTGACAATCC 728
Qy
Db 913 TGAAGATGACAAAGTATACCTTTTCTCGTGAATGCAATAGATGGAAGAACACTCTGG 972
Qy
Db 729 TGAAGATGACAAAGTATACCTTTTCTCGTGAATGCAATAGATGGAAGAACACTCTGG 788
Qy
Db 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGATCTTGGAGGGGACAGAG 1032
Qy
Db 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGATCTTGGAGGGGACAGAG 848
Qy
Db 1033 TCTGGTGAATAAATGACAAACATCTCTCAAAGCTGCTGATTTGCTCAGTGCCAGGTCC 1092
Qy
Db 849 TCTGGTGAATAAATGACAAACATCTCTCAAAGCTGCTGATTTGCTCAGTGCCAGGTCC 908
Qy
Db 1093 AAATGGCATTGACACTCACTTTTGTATGAGTGAAGTGAATTTCTTAATGAACTTTAAAGA 1152
Qy
Db 909 AAATGGCATTGACACTCACTTTTGTATGAGTGAAGTGAATTTCTTAATGAACTTTAAAGA 968
Qy
Db 1153 TCCTAAAAATCCAGTTGATATGAGTGAATTTAGGATTTACGACTTCCAGTAACTTTCAAGGATC 1212
Qy
Db 969 TCCTAAAAATCCAGTTGATATGAGTGAATTTAGGATTTACGACTTCCAGTAACTTTCAAGGATC 1028
Qy
Db 1213 AGCCGTGTATGTATAGCATGAGTGAAGAGGTTTCTTGGTCCATATGCCCA 1272
Qy
Db 1029 AGCCGTGTATGTATAGCATGAGTGAAGAGGTTTCTTGGTCCATATGCCCA 1088
Qy
Db 1273 CAGGATGACCCCAACTATCAATGGGTGCTTTATCAAGGAAGTCCCTATCCACGGCC 1332
Qy
Db 1089 CAGGATGACCCCAACTATCAATGGGTGCTTTATCAAGGAAGTCCCTATCCACGGCC 1148
Qy
Db 1333 AGGAATCTTGTCCAGCAAAACATTTGGTGGTTTGACTCTACAAAGGACCTTCTCTGATGA 1392

Db 1149 AGGAATCTTGTCCAGCAAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTTCTCTGATGA 1208
Qy
Db 1393 TGTATAACCTTTGCAAGAAGTATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA 1452
Qy
Db 1209 TGTATAACCTTTGCAAGAAGTATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA 1268
Qy
Db 1453 TCGCCCAATAGTATCAAAAACGGATGTAATTTATCAATTTACAAATTTGCTGAGACCG 1512
Qy
Db 1269 TCGCCCAATAGTATCAAAAACGGATGTAATTTATCAATTTACAAATTTGCTGAGACCG 1328
Qy
Db 1513 AGTGTATGAGAAAGATGAGACATGTATGTATTTATCGGAAACAGATGTTGGGACCGT 1572
Qy
Db 1329 AGTGTATGAGAAAGATGAGACATGTATGTATTTATCGGAAACAGATGTTGGGACCGT 1388
Qy
Db 1573 TCTTAAAGTAGTTCCTCAATTTCTTAAGGAGACTTTGGTATGATTTAGAAAGAGTTCCTGCTGA 1632
Qy
Db 1389 TCTTAAAGTAGTTCCTCAATTTCTTAAGGAGACTTTGGTATGATTTAGAAAGAGTTCCTGCTGA 1448
Qy
Db 1633 AGAAATGACAGTTCCTCGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1692
Qy
Db 1449 AGAAATGACAGTTCCTCGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508
Qy
Db 1693 GCACCAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACCGGTGTGA 1752
Qy
Db 1509 GCACCAACTATATATTTGGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACCGGTGTGA 1568
Qy
Db 1753 TATTTACGGGAAAGCGTGTGCTGAGTTCCTCGCCCGAGACCTTACTGTCTGGGA 1812
Qy
Db 1569 TATTTACGGGAAAGCGTGTGCTGAGTTCCTCGCCCGAGACCTTACTGTCTGGGA 1628
Qy
Db 1813 TGGTTCTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGACGCAAGACGACAAGATAT 1872
Qy
Db 1629 TGGTTCTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGACGCAAGACGACAAGATAT 1688
Qy
Db 1873 TGAAGATGGAGACCACTGACTCATCTGTTTACAGCTTTACACCATGATAATCACCATTGGCCA 1932
Qy
Db 1689 TGAAGATGGAGACCACTGACTCATCTGTTTACAGCTTTACACCATGATAATCACCATTGGCCA 1748
Qy
Db 1933 CAGCCCTGAAAGAGAGATCATCTATGGTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1992
Qy
Db 1749 CAGCCCTGAAAGAGAGATCATCTATGGTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1808
Qy
Db 1993 TCCGAAGTGCAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAAGAGCGAAA 2052
Qy
Db 1809 TCCGAAGTGCAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGAAATGAAAGAGCGAAA 1868
Qy
Db 2053 AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGGTAG 2112
Qy
Db 1869 AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGGTAG 1928
Qy
Db 2113 TCTACAAACAGAGAGATTCAGGCAATTTACTCTGCCATCGGTTGGAAACATGGGTTTATACA 2172
Qy
Db 1929 TCTACAAACAGAGAGATTCAGGCAATTTACTCTGCCATCGGTTGGAAACATGGGTTTATACA 1988
Qy
Db 2173 AACTCTTCTTAAGGTAAACCTTGGAAAGTCAATTTGACACAGAGCAATTTGGAAAGAACTTCTTCA 2232
Qy
Db 1989 AACTCTTCTTAAGGTAAACCTTGGAAAGTCAATTTGACACAGAGCAATTTGGAAAGAACTTCTTCA 2048
Qy
Db 2233 TAAAGATGATGAGAGTGGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2292
Qy
Db 2049 TAAAGATGATGAGAGTGGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2108
Qy
Db 2293 CCAGAAAGTCTGGTACAGAGACTTCATGCAAGTCTCAACACCCCAATCTCAACACGAT 2352
Qy
Db 2109 CCAGAAAGTCTGGTACAGAGACTTCATGCAAGTCTCAACACCCCAATCTCAACACGAT 2168
Qy
Db 2353 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAAAACAACTCGGCAAGGCCAGG 2412
Qy
Db 2169 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAAAACAACTCGGCAAGGCCAGG 2228
Qy
Db 2413 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATATAGAAAGGTAGAAA 2472
Qy
Db 2229 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATATAGAAAGGTAGAAA 2288

QY 2473 CAGGAGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2532
 DB 2299 CAGGAGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2348
 QY 2533 AACCTCAACAGTAGTGAACCTTGGCTAGACAAATACTGGAAAAACAATGCAATATACAT 2592
 DB 2349 AACCTCAACAGTAGTGAACCTTGGCTAGACAAATACTGGAAAAACAATGCAATATACAT 2408
 QY 2593 GAACTTTTTTCATGCGCATATGTGATGTTTACAAATGTTGGAAATTCAGCTGAGTTCCA 2652
 DB 2409 GAACTTTTTTCATGCGCATATGTGATGTTTACAAATGTTGGAAATTCAGCTGAGTTCCA 2469
 QY 2653 CCAATTAATAAATAATCCATCAGTAACCTTCTTAATAGGCTTTTTTTTCC 2702
 DB 2469 CCAATTAATAAATAATCCATCAGTAACCTTCTTAATAGGCTTTTTTTTCC 2518

RESULT 6
 ID ADN95334
 XX ADN95334 standard; DNA; 2530 BP.
 AC ADN95334;
 XX
 DT 01-JUL-2004 (first entry)
 XX Human BEC/LEC-related gene sequence SeqID256.
 DE growth; differentiation; blood endothelial cell; BEC;
 XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;
 KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;
 KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;
 KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;
 KW human.
 XX Homo sapiens.
 XX WO2003080640-A1.
 PN 02-OCT-2003.
 PD 07-MAR-2003; 2003WO-US006900.
 XX 07-MAR-2002; 2002US-0363019P.
 PR (LUDW-) LUDWIG INST CANCER RES.
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
 XX WPI: 2003-876899/81.
 DR P-PSDB; ADN95333.
 PS
 XX Example 1; SEQ ID NO 256; 176pp; English.

This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprising contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a

CC medicament for the differential modulation of blood vessel endothelial cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the CC indexer using the source data given in table 14 of the specification.

XX Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;
 SQ Query Match 92.6%; Score 2508.4; DB 11; Length 2530;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGAGTATTACTTACAGC 252
 DB 9 CTGAGCATGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGAGTATTACTTACAGC 68
 QY 253 AAGAGCAAACTATCAGAAATGGAAACAATGTGCCAAGGCTGAAATTTATCTACAAAGA 312
 DB 69 AAGAGCAAACTATCAGAAATGGAAACAATGTGCCAAGGCTGAAATTTATCTACAAAGA 128
 QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
 DB 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
 QY 373 TACCTTCCTTTTGGATGAGGAACGGAGTAGCTGTATGTTGGAGCAAAAGGATCATAATT 432
 DB 189 TACCTTCCTTTTGGATGAGGAACGGAGTAGCTGTATGTTGGAGCAAAAGGATCATAATT 248
 QY 433 TTCAATCCACCTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
 DB 249 TTCAATCCACCTGGTTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308
 QY 493 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTCAT 552
 DB 309 CAGAAGAGATGAATGCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTCAT 368
 QY 553 CAAGTACTTAAAGCATATATCAGACTCACTTTGACGCTGTGAAACGGGGCTTTTCA 612
 DB 369 CAAGTACTTAAAGCATATATCAGACTCACTTTGACGCTGTGAAACGGGGCTTTTCA 428
 QY 613 TCCAAATTTGACCTTAAATTTGAAATTTGACATCATCTCTGAGGACATATTTTAAAGCTGGA 672
 DB 429 TCCAAATTTGACCTTAAATTTGAAATTTGACATCATCTCTGAGGACATATTTTAAAGCTGGA 488
 QY 673 GAACTCACAATTTTGAACACGGCCGGTGGAAAGAGTCCATATGACCTAAAGCTGCTGACAGC 732
 DB 489 GAACTCACAATTTTGAACACGGCCGGTGGAAAGAGTCCATATGACCTAAAGCTGCTGACAGC 548
 QY 733 ATCCCTTTTAAATAGATGAGAAATTTATCTCTGGAATCTGAGTATTTTGGGGCGAGA 792
 DB 549 ATCCCTTTTAAATAGATGAGAAATTTATCTCTGGAATCTGAGTATTTTGGGGCGAGA 608
 QY 793 CTTTGTCTATCTTCCGAACTCTTTGGGCACCAACACCAATTCAGGACAGAGCATGATTC 852
 DB 609 CTTTGTCTATCTTCCGAACTCTTTGGGCACCAACCAATTCAGGACAGAGCATGATTC 668
 QY 853 CAGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCCACTCATCTCAGAGAGTGACAATCC 912
 DB 669 CAGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCCACTCATCTCAGAGAGTGACAATCC 728
 QY 913 TGAAGATCAAAAGTATATCTTTCTCCGTGAAATCCAAATTCAGATGAGAGACACTCTCG 972
 DB 729 TGAAGATCAAAAGTATATCTTTCTCCGTGAAATCCAAATTCAGATGAGAGACACTCTCG 788
 QY 973 AAAAGCTACTCAGCTAGATAGGTCAGATATGCAAGATGACTTTTGAGGGGCACAGAAG 1032
 DB 789 AAAAGCTACTCAGCTAGATAGGTCAGATATGCAAGATGACTTTTGAGGGGCACAGAAG 848

XX Example 2; SEQ ID NO 2569; 210pp; English.

PS The invention relates to a novel method for detecting soft tissue sarcoma

CC which comprises obtaining a first soft tissue sample from an individual

CC and a normal soft tissue sample from the same or different individual,

CC determining the expression of a gene in both samples and comparing the

CC expression of the gene in both soft tissue samples, where a higher level

CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has

CC cytostatic applications and may be useful for detecting soft tissue

CC sarcoma, possibly via gene therapy or vaccine production. The nucleic

CC acid sequences may be useful in diagnostic and screening applications.

CC The current sequence is that of a human soft tissue sarcoma-upregulated

CC DNA of the invention. The current sequence is not shown within the

CC specification per se but was submitted in CD format by the inventor.

XX

SQ Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 U; 0 Other;

Query Match 92.6%; Score 2508.4; DB 12; Length 2530;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 252

DB 9 CTGAGCATGGCTGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 68

QY 253 AAGACAACTATCAGATGGGAGGAAACAATGCGCAAGGCTGAATATCTTACAAAGA 312

DB 69 AAGACAACTATCAGATGGGAGGAAACAATGCGCAAGGCTGAATATCTTACAAAGA 128

QY 313 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA 372

DB 129 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA 188

QY 373 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAAAGGATCAATATT 432

DB 189 TACCTTCCTTTTGGATGAGGAACGAGTAGGCTGTATGTTGAGCAAAAGGATCAATATT 248

QY 433 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGCGCAGTATCTTACAC 492

DB 249 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGTTGCGCAGTATCTTACAC 308

QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT 552

DB 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGATGTCTAAATTTCAAT 368

QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGCTTTTCA 612

DB 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGAAACGGGGCTTTTCA 428

QY 613 TCCAAATTCACCTACATGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 672

DB 429 TCCAAATTCACCTACATGAATTTGGACATCATCTGAGGACATATTTTAAAGCTGA 488

QY 673 GAACTCACAATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGC 732

DB 489 GAACTCACAATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTCTGACAGC 548

QY 733 ATCCCTTTTAAATAGATGGAGAATTACTCTGGAATCTGAGCTGATTTTATGCGGCGAGA 792

DB 549 ATCCCTTTTAAATAGATGGAGAATTACTCTGGAATCTGAGCTGATTTTATGCGGCGAGA 608

QY 793 CTTTGTCTATCTTCGACACTTTGGGACCAACCAACCAATCATCAGACAGCAGCATGATTC 852

DB 609 CTTTGTCTATCTTCGACACTTTGGGACCAACCAACCAATCATCAGACAGCAGCATGATTC 668

QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATAGTGCACCACTCATCTCAGAGAGTGACAATCC 912

DB 669 CAGGTGGCTCAATGATCCAAAGTTCAATAGTGCACCACTCATCTCAGAGAGTGACAATCC 728

QY 913 TGAAGATGACAAAGTATATCTTTTCTTCCTCGTGAATGCAATAGATGGAGAACATCTGG 972

DB 729 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAGAACACTCTGG 788

QY 973 AAAAGCTACTCACCTAGAAATAGCTCAGATATGCAAGAATGACTTTTGAGGGGCACAGAAG 1032

DB 789 AAAAGCTACTCACCTAGAAATAGCTCAGATATGCAAGAATGACTTTTGAGGGGCACAGAAG 848

QY 1033 TCTGGTGAATAAATGGGACAACTTCTCTCAAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 1092

DB 849 TCTGGTGAATAAATGGGACAACTTCTCTCAAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 908

QY 1093 AAAATGGCATTCACACTCAATTTTGTATGATGACGAGTATGATTCCTTAATGAACTTTTAAAGA 1152

DB 909 AAAATGGCATTCACACTCAATTTTGTATGATGACGAGTATGATTCCTTAATGAACTTTTAAAGA 968

QY 1153 TCCTAAAATCCAGTTGTATATGAGTGTTCACGACTTCCAGTAACATTTTCAAGGGATC 1212

DB 969 TCCTAAAATCCAGTTGTATATGAGTGTTCACGACTTCCAGTAACATTTTCAAGGGATC 1028

QY 1213 AGCCGTGTATGATATAGCATGATGATGAGAGGGTGTTCCTTGTGTCATATGCCCA 1272

DB 1029 AGCCGTGTATGATATAGCATGATGATGAGAGGGTGTTCCTTGTGTCATATGCCCA 1088

QY 1273 CAGGGATGGACCCCAACTACTCAATGGTGCCTTATCAGGAAGAGTCCCTTATCCACGGCC 1332

DB 1089 CAGGGATGGACCCCAACTACTCAATGGTGCCTTATCAGGAAGAGTCCCTTATCCACGGCC 1148

QY 1333 AGGAACTTGTCCAGCAAAACATTTTGGTGGTGTTCGACTTACAAAGGACCTTCTCTGATGA 1392

DB 1149 AGGAACTTGTCCAGCAAAACATTTTGGTGGTGTTCGACTTACAAAGGACCTTCTCTGATGA 1208

QY 1393 TGTATATAACCTTTGCAAGAAGTCATCCAGCCATGTATCAATCAAGTGTTCCTATGAAACA 1452

DB 1209 TGTATATAACCTTTGCAAGAAGTCATCCAGCCATGTATCAATCAAGTGTTCCTATGAAACA 1268

QY 1453 TCGCCCAATAGTATCAAAACGGATGTAATTAATTAATTTACAAATTTGCTGTAGACCG 1512

DB 1269 TCGCCCAATAGTATCAAAACGGATGTAATTAATTAATTTACAAATTTGCTGTAGACCG 1328

QY 1513 AGTGATGACGAAGATGACAGATGATGATGTTATGTTATCGGAAACAGATGTTGGACCGT 1572

DB 1329 AGTGATGACGAAGATGACAGATGATGATGTTATGTTATCGGAAACAGATGTTGGACCGT 1388

QY 1573 TCTTAAAGTAGTTTCAATTCCTAAAGGACATTTGGTATGATTAATTTAGAAAGGTTCTCTGGA 1632

DB 1389 TCTTAAAGTAGTTTCAATTCCTAAAGGACATTTGGTATGATTAATTTAGAAAGGTTCTCTGGA 1448

QY 1633 AGAATGACAGTTCCTGGGAAACCGACTGCTATTTTACGAATGAGGCTTCCACTAAGCA 1692

DB 1449 AGAATGACAGTTCCTGGGAAACCGACTGCTATTTTACGAATGAGGCTTCCACTAAGCA 1508

QY 1693 GCAACAACTATATTTGGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGGA 1752

DB 1509 GCAACAACTATATTTGGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGGA 1568

QY 1753 TATTTACGGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTATCTGTGCTGGGA 1812

DB 1569 TATTTACGGGAAAGCGTGTCTGAGTGTTCCTCGCCGAGACCTTATCTGTGCTGGGA 1628

QY 1813 TGGTTCGTCTGCTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGCAAGATAT 1872

DB 1629 TGGTTCGTCTGCTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGCAAGATAT 1688

QY 1873 AAGAAATGGAGACCCACTGACTCACTGTTTACAGACTTACACCATGATAATCACCATGGCCA 1932

DB 1689 AAGAAATGGAGACCCACTGACTCACTGTTTACAGCTTACACCATGATAATCACCATGGCCA 1748

QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCG 1992

DB 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCG 1808

QY 1993 TCCGAGTCCGAGAGAGCGCTGTTTATTTGCAATTTCCAGAGCGGCAATAGAGAGCGAA 2052

DB 1809 TCCGAGTCCGAGAGAGCGCTGTTTATTTGGCAATTTCCAGAGCGGCAATAGAGAGCGAA 1868

QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTACGTAG 2112
 DB 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTACGTAG 1928
 QY 2113 TCTACACAGAGAGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGTTTCATCA 2172
 DB 1929 TCTACACAGAGAGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGTTTCATCA 1988
 QY 2173 AACTCTTCTTAAGTAAACCTCGAAGTCATTGACACAGAGCAATTTGGAAAGCAATCTTCTCA 2232
 DB 1989 AACTCTTCTTAAGTAAACCTCGAAGTCATTGACACAGAGCAATTTGGAAAGCAATCTTCTCA 2048
 QY 2233 TAAAGATGATGATGAGATGGCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
 DB 2049 TAAAGATGATGATGAGATGGCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
 QY 2293 CCAGAAGTCTGGTACAGAGATTCATGACAGTCTATCAACACCCCAATCTCAACACGAT 2352
 DB 2109 CCAGAAGTCTGGTACAGAGATTCATGACAGTCTATCAACACCCCAATCTCAACACGAT 2168
 QY 2353 GGATGAGTCTCTGAACCAAGTTTGAAGAGGACCGAAACCAACCTCGCAAGGCCAGG 2412
 DB 2169 GGATGAGTCTCTGAACCAAGTTTGAAGAGGACCGAAACCAACCTCGCAAGGCCAGG 2228
 QY 2413 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAA 2472
 DB 2229 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAA 2288
 QY 2473 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA 2532
 DB 2289 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGTGCATTAACCTCTAGA 2348
 QY 2533 AACCTCAACCAAGTAAAGTCTGCTAGCAATACTGGAACCAATGGAAGCAATGCAATATACAT 2592
 DB 2349 AACCTCAACCAAGTAAAGTCTGCTAGCAATACTGGAACCAATGGAAGCAATGCAATATACAT 2408
 QY 2593 GAACTTTTTCATGCGCATTTATGATGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2652
 DB 2409 GAACTTTTTCATGCGCATTTATGATGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2468
 QY 2653 CCAATTAATAATCAATCAATGAGTAACTTTCTCTAATAGGCTTTTTTTC 2702
 DB 2469 CCAATTAATAATCAATCAATGAGTAACTTTCTCTAATAGGCTTTTTTTC 2518

RESULT 8

AAQ87442
 ID AAQ87442 standard; cDNA; 2601 BP.
 AC AAQ87442;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-NOV-1995 (first entry)
 XX
 DE Human semaphorin III cDNA.
 XX Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium;
 KW variola major virus; smallpox; semaphorin receptor binding activity;
 KW modulation; nerve cell growth; immune response; viral pathogenesis;
 KW neurological disease; neuro-regeneration; oncological infection; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 16..2331
 FT CDS /*tag= a
 FT /product= "human semaphorin III"
 XX
 XX WO9507706-Al.
 XX 23-MAR-1995.
 XX

PF 13-SEP-1994; 94WO-US010151.
 XX
 PR 13-SEP-1993; 93US-00121713.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Goodman CS, Kolodkin AL, Matthes D, Bentley DR, O'Connor T;
 DR WPI; 1995-131177/17.
 XX
 DR P-PSDB; AAR71380.
 XX
 PT New class of semaphorin peptide(s) and polypeptide(s) - are potent
 PT modulators of nerve cell growth and regeneration.
 XX
 PS Example 2; Page 60-63; 101pp; English.
 XX
 CC The sequence of the cDNA encoding the human semaphorin III protein. The
 CC proteins encoded by the grasshopper semaphorin I (AAQ87441), human
 CC semaphorin III, vaccinia virus semaphorin IV (AAQ87443), Drosophila
 CC semaphorin I and II (AAQ87444-5), Tribolium semaphorin I (AAQ87446) or
 CC variola major (smallpox) virus semaphorin IV (AAQ87447) genes were used
 CC to generate a series of peptides (AAR70370-R70418), which retain
 CC semaphorin receptor binding activity. The semaphorin derived or
 CC semaphorin receptor derived peptides are potent modulators of nerve cell
 CC growth, immune responsiveness and viral pathogenesis. They can be used in
 CC diagnosis and treatment of neurological disease and neuro-regeneration,
 CC immune modulation and diagnosis and treatment of viral and oncological
 CC infection and diseases. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 2601 BP; 809 A; 533 C; 593 G; 666 T; 0 U; 0 Other;
 Query Match 92.6%; Score 2508.4; DB 2; Length 2601;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 193 CTGACGATGGCTGGTTAACTAGATTTCTGCTCTTTCTGGGAGTATTACTTACAGC 252
 DB 9 CTGACGATGGCTGGTTAACTAGATTTCTGCTCTTTCTGGGAGTATTACTTACAGC 68
 QY 253 AAGACCAACTATCAGAATGGGAACAACAATGTGCAAGGCTGAAATATCTTACAAAGA 312
 DB 69 AAGACCAACTATCAGAATGGGAACAACAATGTGCAAGGCTGAAATATCTTACAAAGA 128
 QY 313 AATGTTGAAATCCAAATGTGATCATCTTCAATGGTGGCCAAACAGCTCCAGTTATCA 372
 DB 129 AATGTTGAAATCCAAATGTGATCATCTTCAATGGTGGCCAAACAGCTCCAGTTATCA 188
 QY 373 TACCTTCTTTTGGATGAGGACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
 DB 189 TACCTTCTTTTGGATGAGGACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
 QY 433 TTCATTGACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACAC 492
 DB 249 TTCATTGACCTGGTTAATATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACAC 308
 QY 493 CAGAAGAGATGAATCCAAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTCAT 552
 DB 309 CAGAAGAGATGAATCCAAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTCAT 368
 QY 553 CAGGATCTTAAGGATATATACAGACTCAGTGTACGCTGTGAAACGGGGCTTTTCA 612
 DB 369 CAGGATCTTAAGGATATATACAGACTCAGTGTACGCTGTGAAACGGGGCTTTTCA 428
 QY 613 TCCAAATTTGACCTACATTTGAATTTGGACATCATCTCTGAGGACATATTTTTTAAGCTGA 672
 DB 429 TCCAAATTTGACCTACATTTGAATTTGGACATCATCTCTGAGGACATATTTTTTAAGCTGA 488
 QY 673 GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 732
 DB 489 GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 548
 QY 733 ATCCCTTTTATAGATGGGAATTTATCTCTGGAATGAGTATTATCTGGAATGAGTATTATGGGGGAGA 792

Db 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGA 608
 Qy 793 CTTTGTATCTTCGGAACCTCTTGGGACACCAACCAATCAGGACAGAGCAGCATGATTC 852
 Db 609 CTTTGTATCTTCGGAACCTCTTGGGACACCAACCAATCAGGACAGAGCAGCATGATTC 668
 Qy 853 CAGGTGGCTCAATGATCCAAAGTTCATTAAGTCCCACTCTCTCAGAGAGTGACAATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTAAGTCCCACTCTCTCAGAGAGTGACAATCC 728
 Qy 913 TGAAGATGACAAAGTATATCTTTCTTCGCGTGAAGTCAATAGATGAGAGAACACTCTGG 972
 Db 729 TGAAGATGACAAAGTATATCTTTCTTCGCGTGAAGTCAATAGATGAGAGAACACTCTGG 788
 Qy 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGATGCTCAGTCCAGGTCC 1032
 Db 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGATGATGCTCAGTCCAGGTCC 848
 Qy 1033 TCTGTGTAATAATGACAAATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCC 1092
 Db 849 TCTGTGTAATAATGACAAATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCC 908
 Qy 1093 AAATGGCATGTGACATCTATTTTGTGAACATGCGAGATGATTTCTTAATGAACCTTTAAAGA 1152
 Db 909 AAATGGCATGTGACATCTATTTTGTGAACATGCGAGATGATTTCTTAATGAACCTTTAAAGA 968
 Qy 1153 TCCTAAATAATCCAGTTGTATATGAGTGTGTTACGACTTCCAGTACATTTTCAAGGGATC 1212
 Db 969 TCCTAAATAATCCAGTTGTATATGAGTGTGTTACGACTTCCAGTACATTTTCAAGGGATC 1028
 Qy 1213 AGCCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1272
 Db 1029 AGCCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1088
 Qy 1273 CAGGATGGAACCAACTATCAATGGTGTCTTATCAAGAGAGTCCCTATCCAGGCC 1332
 Db 1089 CAGGATGGAACCAACTATCAATGGTGTCTTATCAAGAGAGTCCCTATCCAGGCC 1148
 Qy 1333 AGGAATCTGTCCAGCAAAACATTTGGTGTGTTTACACTCAAGAGGACCTTCTGTATGA 1392
 Db 1149 AGGAATCTGTCCAGCAAAACATTTGGTGTGTTTACACTCAAGAGGACCTTCTGTATGA 1208
 Qy 1393 TGTATATAACCTTTGCAAGAAGTCACTCCAGCATGTACCAATCCAGTGTCTTCTATGAACA 1452
 Db 1209 TGTATATAACCTTTGCAAGAAGTCACTCCAGCATGTACCAATCCAGTGTCTTCTATGAACA 1268
 Qy 1453 TCGCCCAATAGTATGATCAAAACCGATGTAAATTAATCAATTTACAAATGTGCTAGACCG 1512
 Db 1269 TCGCCCAATAGTATGATCAAAACCGATGTAAATTAATCAATTTACAAATGTGCTAGACCG 1328
 Qy 1513 AGTGGATCGAAGATGACAGATGATGATGTTATGTTATCGGAACAGATGTGGACCGT 1572
 Db 1329 AGTGGATCGAAGATGACAGATGATGATGTTATGTTATCGGAACAGATGTGGACCGT 1388
 Qy 1573 TCTTAAAGTAGTTTCAATTTCTTAAGGACCTTGGTATGATTTAGAAAGGTTCTCTGGA 1632
 Db 1389 TCTTAAAGTAGTTTCAATTTCTTAAGGACCTTGGTATGATTTAGAAAGGTTCTCTGGA 1448
 Qy 1633 AGAAATGACAGTTTTCGGGAACCGACTGCTATTTTACAGCAATGGAGCTTTCCACTAAGCA 1692
 Db 1449 AGAAATGACAGTTTTCGGGAACCGACTGCTATTTTACAGCAATGGAGCTTTCCACTAAGCA 1508
 Qy 1693 GCAACAACTATATATTTGTTTCAACCGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGGA 1752
 Db 1509 GCAACAACTATATATTTGTTTCAACCGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGGA 1568
 Qy 1753 TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTTACTGTGCTTGGGA 1812
 Db 1569 TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTTACTGTGCTTGGGA 1628
 Qy 1813 TGGTTCTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGCAAGATAT 1872
 Db 1629 TGGTTCTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAACAGCAGCAAGATAT 1688

Qy 1873 AAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTTACCATGATAATCACCATGGCCA 1932
 Db 1689 AAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTTACCATGATAATCACCATGGCCA 1748
 Qy 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1992
 Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCAATTTTGGAAATGCAG 1808
 Qy 1993 TCCGAAGTCCGAGAGAGCGCTGTTCTATTGGCAATTTCCAGAGGGGAAATGAAGAGCGAAA 2052
 Db 1809 TCCGAAGTCCGAGAGAGCGCTGTTCTATTGGCAATTTCCAGAGGGGAAATGAAGAGCGAAA 1868
 Qy 2053 AGAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGCCCTTCTGCTACGTAG 2112
 Db 1869 AGAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGCCCTTCTGCTACGTAG 1928
 Qy 2113 TCTACAAACAGAGAGATTCAGGCAATTTACTCTGCCATCGGTGGAAATCATGGTTTCATACA 2172
 Db 1929 TCTACAAACAGAGAGATTCAGGCAATTTACTCTGCCATCGGTGGAAATCATGGTTTCATACA 1988
 Qy 2173 AACTCTTCTTAAGGTAAACCTTGGAAAGTCAATTTGACACAGAGCAATTTGGAAAGCACTTCTTCA 2232
 Db 1989 AACTCTTCTTAAGGTAAACCTTGGAAAGTCAATTTGACACAGAGCAATTTGGAAAGCACTTCTTCA 2048
 Qy 2233 TAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCATAGCATGACACCTAG 2292
 Db 2049 TAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCATAGCATGACACCTAG 2108
 Qy 2293 CCAGAAGTCTGTGTACAGAGACTTTCATGCACTCATCAACCAACCCCAATCTCAACACGAT 2352
 Db 2109 CCAGAAGTCTGTGTACAGAGACTTTCATGCACTCATCAACCAACCCCAATCTCAACACGAT 2168
 Qy 2353 GGATGAGTCTGTGAAACAAAGTTTGGAAAGGACCGGAAACAAACGTCGGGAAAGGCCAGG 2412
 Db 2169 GGATGAGTCTGTGAAACAAAGTTTGGAAAGGACCGGAAACAAACGTCGGGAAAGGCCAGG 2228
 Qy 2413 ACATACCCCGGGAACAGTAAACAAATGGAAGCACTTACAAAGAAATAGAAAGGTAGAAA 2472
 Db 2229 ACATACCCCGGGAACAGTAAACAAATGGAAGCACTTACAAAGAAATAGAAAGGTAGAAA 2288
 Qy 2473 CAGGAGACCCCAAGATTTGAGAGGACCCAGAGGTGTCTGAGCTGCATTACCTCTAGA 2532
 Db 2289 CAGGAGACCCCAAGATTTGAGAGGACCCAGAGGTGTCTGAGCTGCATTACCTCTAGA 2348
 Qy 2533 AACCTCAAAACAAAGTAGAAAACCTTGCTGACAAATTAACGAAAAACAAATGCAATATACAT 2592
 Db 2349 AACCTCAAAACAAAGTAGAAAACCTTGCTGACAAATTAACGAAAAACAAATGCAATATACAT 2408
 Qy 2593 GAACTTTTTCATGGCATTTATGTTGATGTTTACAAATGGTGGAAATTCAGCTGAGTTCCA 2652
 Db 2409 GAACTTTTTCATGGCATTTATGTTGATGTTTACAAATGGTGGAAATTCAGCTGAGTTCCA 2468
 Qy 2653 CCAATTATAAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTCCTCC 2702
 Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTCCTCC 2518

RESULT 9

ADQ23894
 ID ADQ23894 standard; DNA; 3023 BP.
 XX ADQ23894;
 AC ADQ23894;
 XX
 DT 26-AUG-2004 (first entry)
 XX Human soft tissue sarcoma-upregulated DNA - SEQ ID 6714.
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 KW soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
 OS ds.
 XX Homo sapiens.
 XX

Db	1569	TATTTACGGGAAGCGGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGA	1628
Qy	1813	TGGTTCTGCAATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCAACAAGATAT	1872
Db	1629	TGGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCAACAAGATAT	1688
Qy	1873	AAGAAATGGAGACCCACTGACTCTGTTTCAGACTTACACCATGATTAATCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCTGTTTCAGACTTACACCATGATTAATCA	1748
Qy	1933	CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTT	1992
Db	1749	CAGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTAGCACATTTT	1808
Qy	1993	TCCGAAGTCGAGAGAGCGCTGTGTTATTTGGCAATTCAGAGGCGAAATGAAG	2052
Db	1809	TCCGAAGTCGAGAGAGCGCTGTGTTATTTGGCAATTCAGAGGCGAAATGAAG	1868
Qy	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGAGACAGATCAAGGCCCTT	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGAGACAGATCAAGGCCCTT	1928
Qy	2113	TCTACAAAGAAAGGATTCAGGCAATTAACCTCTGCGATCGCGTGGAACATGG	2172
Db	1929	TCTACAAAGAAAGGATTCAGGCAATTAACCTCTGCGATCGCGTGGAACATGG	1988
Qy	2173	AACCTCTTTAAAGTAAACCTTGGAAATCATTTGACACAGAGCAATTTGGAAG	2232
Db	1989	AACCTCTTTAAAGTAAACCTTGGAAATCATTTGACACAGAGCAATTTGGAAG	2048
Qy	2233	TAAAGATGATGATGGAGATGGCTCTAGAGACCAAGAAATGTCCTCAATAGCA	2292
Db	2049	TAAAGATGATGATGGAGATGGCTCTAGAGACCAAGAAATGTCCTCAATAGCA	2108
Qy	2293	CCAGAAAGTCTGGTACAGAGACTTCATGACAGCTCATCAACACCCCAATCT	2352
Db	2109	CCAGAAAGTCTGGTACAGAGACTTCATGACAGCTCATCAACACCCCAATCT	2168
Qy	2353	GGATGATTTCTGTGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCG	2412
Db	2169	GGATGATTTCTGTGAAACAAGTTTGGAAAAAGGACCGGAAAAACAACGTCG	2228
Qy	2413	ACATACCCAGGGAAACAGTAACAAATGGAAGCACTTCAAGAAAAATAAGAA	2472
Db	2229	ACATACCCAGGGAAACAGTAACAAATGGAAGCACTTCAAGAAAAATAAGAA	2288
Qy	2473	CAGGAGACCCACGAATTTGAGAGGGCACCCAGAGTGTCTGAGCTGCATTAC	2532
Db	2289	CAGGAGACCCACGAATTTGAGAGGGCACCCAGAGTGTCTGAGCTGCATTAC	2348
Qy	2533	AACCTCAAAACAGTATAGAACTTCGCTAGACAAATACTGGAAAAACAATGC	2592
Db	2349	AACCTCAAAACAGTATAGAACTTCGCTAGACAAATACTGGAAAAACAATGC	2408
Qy	2593	GAACTTTTTTTCATGGCAATTAATGTGGATGTTTACAATGGTGGGAAATTC	2652
Db	2409	GAACTTTTTTTCATGGCAATTAATGTGGATGTTTACAATGGTGGGAAATTC	2468
Qy	2653	CCAATTAATAAATTAATCCCATGAGTAACTTTCTCTAATAGCGTTTTTTTCC	2702
Db	2469	CCAATTAATAAATTAATCCCATGAGTAACTTTCTCTAATAGCGTTTTTTTCC	2518

RESULT 10

RESUL I
AAO92331

AAQ92331
ID AAQ92331 standard; cDNA; 1481 BP.

XX
DT
TCCZCZHHHAA
AC AAO92331:

AC	AAQ92331;
XX	
DT	01-NOV-1995 (first entry)

XX
IN 6667-AON-70 9 78777)

Human collapsin cDNA.

XX		Collapse; antibody; therapy; ds.
KW		Homo sapiens.
OS		
XX		
XX		
PH	Key	Location/Qualifiers
FT	CDS	50..1480
FT		/*tag= a
XX		
PN	US5416197-A.	
XX		
PD	16-MAY-1995.	
XX		
PF	15-OCT-1993;	93US-00136922.
XX		
PR	15-OCT-1993;	93US-00136922.
XX		
PA	(UYPE-) UNIV PENNSYLVANIA.	
XX		
PI	Luo Y, Raper JA;	
XX		
DR	WPI; 1995-193478/25.	
XX	P-PSDB; AAR74175.	
XX		
PT	New antibody to human collapsin - used to inhibit the activity of	
PT	collapsin, to induce neurite out-growth and to treat individuals with	
PT	nerv damage.	
XX		
XX	Disclosure; Col 11-16; 11pp; English.	
XX		
CC	Human collapsin and its encoding nucleic acid may be used to identify	
CC	agents which modulate the ability of human collapsin to collapse the	
CC	growth cone of neurons. An antibody capable of specifically binding at	
CC	least a portion of the collapsin protein can be used to purify human	
CC	collapsin and to inhibit the activity of the protein. It can be used to	
CC	induce neurite outgrowth by neuronal cells and to treat individuals	
CC	suffering from nerve damage	
XX		
SQ	Sequence 1481 BP; 454 A; 299 C; 345 G; 383 T; 0 U; 0 Other;	
	Query Match	52.2%; Score 1415.2; DB 2; Length 1481;
	Best Local Similarity	99.4%; Pred. No. 0;
	Matches 1420; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
Qy	899	GAGAGTGACAATCCTGAAAGATGACAAAGTATATCTTTTCCTCGTGAAAATGCCAATAGAT 958
Db	53	GAACATGACAATCCTGAAGATGACAAAGTATATCTTTTCCTCGTGAAAATGCCAATAGAT 112
Qy	959	GGAGAACACTCTGGAAAAAGCTACTCACGGTAGAATAGGTGCAGATATGCAAGATGACTTT 1018
Db	113	GGAGAACACTCTGGAAAAAGCTACTCACGGTAGAATAGGTGCAGATATGCAAGATGACTTT 172
Qy	1019	GGAGGGCACAGAAGTCTGGTGAATAATGACAAACATTCTCTCAAAGCTCGTCTGATTTCG 1078
Db	173	GGAGGGCACAGAAGTCTGGTGAATAATGGACAAACATTCTCTCAAAGCTCGTCTGATTTCG 232
Qy	1079	TCAGTGCAGGTCACAAATGGCATGTGACATCTATTTTGTGAACTGCAGAGTATTCCTTA 1138
Db	233	TCAGTGCAGGTCACAAATGGCATGTGACATCTATTTTGTGAACTGCAGAGTATTCCTTA 292
Qy	1139	ATGACATTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAAC 1198
Db	293	ATGACATTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAAC 352
Qy	1199	ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGAGTGCATGTGAGAAGGGTGTTCCTT 1258
Db	353	ATTTTCAAGGGATCAGCCGTGTGTATGTATAGCATGAGTGCATGTGAGAAGGGTGTTCCTT 412
Qy	1259	GGTCCATATGCCACAGGGATGACCACACTATCAATGGTGGCTTATCAAGGAAGATC 1318
Db	413	GGTCCATATGCCACAGGGATGACCACACTATCAATGGTGGCTTATCAAGGAAGATC 472
Qy	1319	CCCTATCCAGGGCCAGGAACCTTGTCAGCAAAACATTTGGTGGTTTTGACTCTACAAAG 1378

Db 473 CCTATCCAGCGCCAGAACTTGTCCAGCAAAACATTTGGTGGTTTGTACTCTCAAG 532
 Qy 1379 GACCTTCCTGATGATGTTTATAACCTTTTCAAGAGTTCATCCAGCCATGTACAAATCCAGTG 1438
 Db 533 GACCTTCCTGATGATGTTTATAACCTTTTCAAGAGTTCATCCAGCCATGTACAAATCCAGTG 592
 Qy 1439 TTTCTCTATGAACAATCGCCCAATAGTGATCAAAAACGAGTGAATTAATCAATTTACAAA 1498
 Db 593 TTTCTCTATGAACAATCGCCCAATAGTGATCAAAAACGAGTGAATTAATCAATTTACAAA 652
 Qy 1499 ATTGTCGTAGACCGAGTGCATGACAGAGATGACAGTATGATGTTATGTTATCGGAACA 1558
 Db 653 ATCGTCGTAGACCGAGTGCATGACAGAGATGACAGTATGATGTTATGTTATCGGAACA 712
 Qy 1559 GATGTTGGGACCGCTTCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTAGAA 1618
 Db 713 GATGTTGGGACCGCTTCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTAGAA 772
 Qy 1619 GAGGTTCTGCTGGAAGAAATGACAGTCTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAG 1678
 Db 773 GAGGTTCTGCTGGAAGAAATGACAGTCTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAG 832
 Qy 1679 CTTTCCACTAAGCAGCAACTATATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCT 1738
 Db 833 CTTTCCACTAAGCAGCAACTATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCT 892
 Qy 1739 TTACACCGGTGTGATATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTT 1798
 Db 893 TTACACCGGTGTGATATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGAGACCTT 952
 Qy 1799 TACTGTGCTGGGATGTTTCTGATGTTCTGCTATTTTCCACTGCAAGAGAGCGACA 1858
 Db 953 TACTGTGCTGGGATGTTTCTGATGTTCTGCTATTTTCCACTGCAAGAGAGCGACA 1012
 Qy 1859 AGACGACAGATATAGAATGGAGACCCACTGACTCTGCTGACTTACAGCTTACCATGAT 1918
 Db 1013 AGACGACAGATATAGAATGGAGACCCACTGACTCTGCTGACTTACAGCTTACCATGAT 1072
 Qy 1919 AATCACCATTGGCCACAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACA 1978
 Db 1073 AATCACCATTGGCCACAGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACA 1132
 Qy 1979 TTTTGTGAATGAGTCCGAGTCCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGGCGA 2038
 Db 1133 TTTTGTGAATGAGTCCGAGTCCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGGCGA 1192
 Qy 2039 AATGAAGAGCGAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGC 2098
 Db 1193 AATGAAGAGCGAAAGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGC 1252
 Qy 2099 CTTCTGCTACGTAGTCTCAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGAA 2158
 Db 1253 CTTCTGCTACGTAGTCTCAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGAA 1312
 Qy 2159 CATGGTTCATACAAACTCTTCTTAAGGTAAACCTCGAAGTCAATTCAGACAGAGATTG 2218
 Db 1313 CATGGTTCATACAAACTCTTCTTAAGGTAAACCTCGAAGTCAATTCAGACAGAGATTG 1372
 Qy 2219 GAAGAACTTCTTCAATAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAAT 2278
 Db 1373 GAAGAACTTCTTCAATAAGATGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAAT 1432
 Qy 2279 AGCATGACACCTAGCAGAGGCTGTTGACAGAGCTTTCATGAGCTC 2326
 Db 1433 AGCATGACACCTAGCAGAGGCTGTTGACAGAGCTTTCATGAGCTC 1480

RESULT 11
 AAX89112
 ID AAX89112 standard; DNA; 2331 BP.
 XX
 AC AAX89112;

XX 14-SEP-1999 (first entry)
 DT Human brain tissue-derived polypeptide coding sequence (clone OM007).
 XX Brain tissue; human; bone marrow; umbilical cord venous endothelial cell;
 KW recombinant; diagnosis; treatment; ss.
 XX Homo sapiens.
 XX WO9933873-A1.
 PN 08-JUL-1999.
 PD 25-DEC-1998; 98WO-JP005952.
 PF 26-DEC-1997; 97JP-00358811.
 PR (ONOI) ONO PHARM CO LTD.
 PA Fukushima D, Shibayama S, Tada H;
 PI WPI; 1999-419088/35.
 XX P-PSDB; AAY27127.
 DR New adult human brain tissue-produced polypeptides useful for diagnosis
 XX and treatment.
 PT Claim 4; Page 39-40; 86pp; Japanese.
 PS The invention provides polypeptides (AAY27127-27133) produced by human
 XX adult brain tissue, human bone marrow or a human umbilical cord venous
 CC endothelial cell. Host cells transformed with vectors comprising the
 CC nucleic acids encoding the polypeptides are used for the recombinant
 CC expression of the polypeptides. The polypeptides can be used in
 CC diagnosis, treatment and basic studies, with wide applications in
 CC treatment depending on the activity to be aimed at. Sequences AAX89112-
 CC 125 represent nucleic acids encoding the polypeptides
 XX
 SQ Sequence 2331 BP; 723 A; 476 C; 529 G; 603 T; 0 U; 0 Other;
 Query Match 26.5%; Score 718.6; DB 2; Length 2331;
 Best Local Similarity 61.9%; Pred. No. 1e-205;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
 Qy 269 AATGGGAAGAAACAATGTGCCAAGCTGAAATATCTCAAAAGAAATGTGGAATCCAAAC 328
 Db 109 ACTTTGAGCAAAATATTTCCAGACTCAAGCTAACTCAAGACTTGTCTCTTCAAT 168
 Qy 329 AATGTGATCATTTCATTTGGCTTGGCCCAACAGCTCCAGTTATCATACCTTCTTTGGAT 388
 Db 169 AGCTGTATTCCTTTTGGGTTTCATCAGAGGACTGGATTTTCAAACTCTTCTCTAGAT 228
 Qy 389 GAGGAACGAGTAGCTGTATGTTGGCAAGAGATCAGATATTTTTCATTCGACCTGGTT 448
 Db 229 GAGGAAGAGGCGAGCTGCTCTTGGGAGCCAAAGACCACATCTTTCTACTAGTCTGGTT 288
 Qy 449 AA---TATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACACCAAGAGAGATGAA 505
 Db 289 GACTTAAACAAAATTTTAAAGAAATTTATTTGGCTCTGCGCAAGGACGGTGGAAATTA 348
 Qy 506 TGCAAGTGGCTGGAAAAGACATCTGAAAGAAATGTGCTAAATTTTTCATCAAGGTACTTAAG 565
 Db 349 TGTAAATAGCTGGGAAAGATGCCAATACAGAATGTGCAATTTTCATCAGAGTACTTCAG 408
 Qy 566 GCATATATCAGACTCATTGTACGCTGTGAAACGGGGCTTTTCATCCAATTTGCACC 625
 Db 409 CCTATACAAAACTCACATATATGTGTGGAACCTGGAGCAATTTTCATCAATATGTGGG 468
 Qy 626 TACATTGAAATGGACATCATCTCAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT 685
 Db 469 TATATTGATCTTGGAGTCTCAAGGAGGATATTTATTTCAAACTAGACACAGTAATTTG 528

PR 10-SEP-1998; 98US-0099812P.
 PR 10-SEP-1998; 98US-0099815P.
 PR 10-SEP-1998; 98US-0099816P.
 PR 15-SEP-1998; 98US-0100385P.
 PR 15-SEP-1998; 98US-0100388P.
 PR 15-SEP-1998; 98US-0100390P.
 PR 16-SEP-1998; 98US-0100584P.
 PR 16-SEP-1998; 98US-0100627P.
 PR 16-SEP-1998; 98US-0100661P.
 PR 16-SEP-1998; 98US-0100662P.
 PR 16-SEP-1998; 98US-0100664P.
 PR 17-SEP-1998; 98US-0100683P.
 PR 17-SEP-1998; 98US-0100684P.
 PR 17-SEP-1998; 98US-0100710P.
 PR 17-SEP-1998; 98US-0100711P.
 PR 17-SEP-1998; 98US-0100919P.
 PR 17-SEP-1998; 98US-0100930P.
 PR 18-SEP-1998; 98US-0100848P.
 PR 18-SEP-1998; 98US-0100849P.
 PR 18-SEP-1998; 98US-0101014P.
 PR 18-SEP-1998; 98US-0101068P.
 PR 18-SEP-1998; 98US-0101071P.
 PR 22-SEP-1998; 98US-0101279P.
 PR 23-SEP-1998; 98US-0101471P.
 PR 23-SEP-1998; 98US-0101472P.
 PR 23-SEP-1998; 98US-0101473P.
 PR 23-SEP-1998; 98US-0101475P.
 PR 23-SEP-1998; 98US-0101476P.
 PR 23-SEP-1998; 98US-0101477P.
 PR 23-SEP-1998; 98US-0101479P.
 PR 24-SEP-1998; 98US-0101738P.
 PR 24-SEP-1998; 98US-0101741P.
 PR 24-SEP-1998; 98US-0101743P.
 PR 24-SEP-1998; 98US-0101915P.
 PR 24-SEP-1998; 98US-0101916P.
 PR 29-SEP-1998; 98US-0102207P.
 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.
 PR 29-SEP-1998; 98US-0102331P.
 PR 30-SEP-1998; 98US-0102484P.
 PR 30-SEP-1998; 98US-0102487P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 30-SEP-1998; 98US-0102571P.
 PR 01-OCT-1998; 98US-0102684P.
 PR 01-OCT-1998; 98US-0102687P.
 PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
 PR 07-OCT-1998; 98US-0103328P.
 PR 07-OCT-1998; 98US-0103359P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
 PR 08-OCT-1998; 98US-0103679P.
 PR 08-OCT-1998; 98US-0103711P.
 PR 14-OCT-1998; 98US-0104257P.
 PR 20-OCT-1998; 98US-0104987P.
 PR 20-OCT-1998; 98US-0105000P.
 PR 20-OCT-1998; 98US-0105002P.
 PR 21-OCT-1998; 98US-0105104P.
 PR 22-OCT-1998; 98US-0105169P.
 PR 22-OCT-1998; 98US-0105266P.
 PR 26-OCT-1998; 98US-0105693P.
 PR 26-OCT-1998; 98US-0105694P.
 PR 27-OCT-1998; 98US-0105807P.
 PR 27-OCT-1998; 98US-0105881P.
 PR 27-OCT-1998; 98US-0105882P.
 PR 28-OCT-1998; 98US-0106023P.

PR 28-OCT-1998; 98US-0106029P.
 PR 28-OCT-1998; 98US-0106030P.
 PR 28-OCT-1998; 98US-0106032P.
 PR 28-OCT-1998; 98US-0106033P.
 PR 28-OCT-1998; 98US-0106178P.
 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
 PR 30-OCT-1998; 98US-0108644P.
 PR 03-NOV-1998; 98US-0108656P.
 PR 03-NOV-1998; 98US-0108902P.
 PR 03-NOV-1998; 98US-0106905P.
 PR 03-NOV-1998; 98US-0106919P.
 PR 03-NOV-1998; 98US-0106932P.
 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
 PR 17-NOV-1998; 98US-0108801P.
 PR 17-NOV-1998; 98US-0108802P.
 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.

XX (GETH) GENENTECH INC.

XX Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;

XX WPI; 2000-237871/20.

XX P-PSDB; AAY99427.

XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small
 PT molecule inhibitors of the relevant receptor/ligand interactions.

XX Claim 2; Fig 175; 773pp; English.

XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention

SQ Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;

Query Match 26.5%; Score 718.6; DB 3; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 1.4e-205;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGAGAACAAATGTGCCAGGCTGAATATCTCTACAGAAATGTGGAAATCAAC 328
 Db 215 ACTTTGAGCAAAATATTCAGACTCAAGCTACCTACAGAACTGTGCTTCAAT 274
 QY 329 AATGTGATCACTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTCTTTGGAT 388
 Db 275 AGCTGATTCCTCTTTTGGGTTTCATCAGAGGACTGGATTTTCAAACTCTCTTAGAT 334
 QY 389 GAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCATATTTTCATTCGACCTGGTT 448
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 335 GAGGAAAGAGGAGGCTGCTCTTTGGAGGACCAAGACCACATCTTCTACTCAGTCTGGTT 394
 Qy 449 AA---TATCAAGAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAA 505
 Db 395 GACTTAACAAAATTTTAAAGAGATTTATTTGGCTGCTGCAAGGAGGCTGGAATTA 454
 Qy 506 TCAAGTGGGCTGGAAGACATCTTGAAGAAATGTCTTAATTTTATCAAGAGTACTTAAG 565
 Db 455 TGTAAATAGCTGGGAAGAGTCCCAATACAGAATGTGCAAAATTTTATCAGAGTACTTCAG 514
 Qy 566 GCATATAATCAGACTCAGCTTGTACGGCTGTGAAAGGGGGCTTTTATCCAAATTTGACCC 625
 Db 515 CCCTATAACAAATTTTATGTTGTGGAATGTGTTGGAATGTGGAATTTTATCCAAATTTG 574
 Qy 626 TACATTGAAATTTGGACATCATCTCAGGACAAATATTTTAAAGCTGGAGAACTCACAATTT 685
 Db 575 TATATTGATCTTGGAGTCTAAGAGAGATTTATTTTCAAATCTAGACACATATTTG 634
 Qy 686 GAAACGGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATA 745
 Db 635 GAGTCTGGCAGACTGAAATGTCTTTCGATCTCAGCAGCCCTTTTGTCTCAGTAATGACA 694
 Qy 746 GATGAGAAATATATCTCTGGAATCTGAGCTGATTTTATGGGGGAGACTTTTCTATCTTC 805
 Db 695 GATGAGTACTCTACTCTGGAACAGCTTCTGATTTTCTTTGGCAAGAGTACTGCATTCAT 754
 Qy 806 CGAATCTTTGGGCT 856
 Db 755 CGATCCCTTTGGGCT 814
 Qy 857 TGGCTCAATGATCCAAAGTTCATTTAGTGGCCCACTCATCTCAGAGAGTGACAAATCCTGAA 916
 Db 815 TGGCTCAATGAGGAGCAAAATTTTATTTGGAATCTTCTCTCTCTCTCTCTCTCTCTCTCT 874
 Qy 917 GATGACAAAGTATCTTTTCTCGTGAAATGCAATAGATGGAGAGACACTCTGGAATA 976
 Db 875 GATGATAAAATATATTTCT 934
 Qy 977 GCTACTCAGCTAGATAGTGCAGATATGCAAGATGACTTTTGGAGGGGACAGAGAGTCTG 1036
 Db 935 ACATCTCTTCTCGAGTTGGAGAGTGTGTAGAAATGATGTAGGAGGACAGCGAGCTG 994
 Qy 1037 GTGAATAAATGACAACTTCTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAAT 1096
 Db 995 ATAAACAAGTGCAGACTTTTCTTAAGGCCAGACTGATTTGCTCAATCTCTGGAAGTAT 1054
 Qy 1097 GCATTTGACACTTATTTGATGAATCTGAGAGTATTCCTTAATGAACTTTAAAGATCCT 1156
 Db 1055 GGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAACAGAGATGAA 1114
 Qy 1157 AAAAATCCAGTTGATATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAG 1216
 Db 1115 AGAAATCCGTAGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGTATGAGTGT 1174
 Qy 1217 GTGTGTATGTATGATGATGTGAGAGGGTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1276
 Db 1175 GTTTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1234
 Qy 1277 GATGACCACTATCATTTGAGTGTGCTTATCAAGAGAGTGTGCTTATCAGCGGCGAGGA 1336
 Db 1235 GAAAGTGCAGACCATCTGTTGGGTGAGTATGATGAGGAGAAATTCCTTATCCACGGCTGCT 1294
 Qy 1337 ACTGTGCTCCAGCAAAACATTTG---GTGTTTTGACTCTACAAAGGAGCTTCTCTGATGAT 1393
 Db 1295 ACATGTCCAGCAAAACCTATGACCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
 Qy 1394 GTTATAACCTTTGCAAGAGTATCCAGCCATGTACAAATCCAGTGTCTTCTATGAACAAT 1453
 Db 1355 GTCATCAGTTTCAAAAGCGGCACTCTGTGATGTATGATGATGATGATGATGATGATGATGAT 1414
 Qy 1454 CCCCCAATAGTATCAAAACGAGTAAATTTATCAATTTACAAATTTGTGTAGACCGA 1513
 Db 1415 GGACCAACGTTCAAGAGAAATCAATGTGGATTAACAGACTGACAGATAGTGTGTGATCAT 1474

Qy 1514 CTGGATGCAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTTGGGACCGTT 1573
 Db 1475 GTCTTGCAGAGATGGCCAGTACGATGATGTTTCTTGGGAACAGACATTTGGAATGTC 1534
 Qy 1574 CTTAAAGTAGTTTCAATTTCTTAAGAGACTTGGTATGATTTTGAAGAGGTTCTGCTGAA 1633
 Db 1535 CTCAAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGTGTGCTGGAG 1591
 Qy 1634 GAAATGACAGTTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCAG 1693
 Db 1592 GAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTTCTCTCTGAAGCAG 1651
 Qy 1694 CAACAATCATATATTTGGTTTCAACGCGTGGGCTTCCAGCTCCCTTTTACACCGGTGTGAT 1753
 Db 1652 CAACAAATTTGATATTTGGTTCCGAGATGATTTAGTTTCACTCTCTCTGCAAGATGCGAC 1711
 Qy 1754 ATTTACGGGAAGCGTGTGCTGAGTGTTCCTGCGCCGAGACCTTACTGTCTTGGAT 1813
 Db 1712 ACTTATGGGAAGCTTTGGCAGACTGTTGTCTTGCAGAGACCCCTACTGTGCTGCGAT 1771
 Qy 1814 GGTCTGCTGATCTCTGCTATTTTCCCACTGCAAGAGACGCAACAGACGACAGATATA 1873
 Db 1772 GGAATGCTATGCTCTCGATATGCTCTTCTTAAAGGAGAGCTAGACGCCAAGATGTA 1831
 Qy 1874 AGAATGAGAGACCACTGACTCAGTCTTTCAGACTTACACCATGATAATCACCATGGCCAC 1933
 Db 1832 AAATATGCGACCCCAATCACCAGTCTGGGACATCGAAGACAGCATTTAGTCAIG---AA 1888
 Qy 1934 AGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATGCA 1993
 Db 1889 ACTGCTGATGAAAGGTTGATTTTGGCATTTGAAATTTAACTCAACCTTTCTGGAATGATA 1948
 Qy 1994 CCGAAGTCCGAGAGAGCGCTGCTCTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 2053
 Db 1949 CCTAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTGAGGAGTGAAGATCGA 2008
 Qy 2054 GAAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGT 2113
 Db 2009 GAGGAGTTGAAGCCCGATGAAAGATCATCAACGGAAATATGGCTACTGATTCGAAGT 2068
 Qy 2114 CTACAACAGAGAGATTCAGGCAATTAATCTCTGCAATGCGGTGGAAACATGGGTTCTATA 2173
 Db 2069 TTGCAAGAGAGAGATTTCTGGATGATTTACTGCAAAAGCCAGAGACACATTTTATCCAC 2128
 Qy 2174 ACTCTTCTTAAGTAAACCTGGAAGTCAATTCACACAGAGCATTTTGGAGAACTTCTTCAT 2233
 Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCTTGAATGAATGAACAGATGGAATAATACCCAGAG 2188
 Qy 2234 AAAGATGATGATG 2246
 Db 2189 GCAGAGCATGAGG 2201

RESULT 13
 AAF54421
 ID AAF54421 standard; DNA; 3871 BP.
 XX
 AC AAF54421;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE DNA encoding protein of the invention #86.
 XX
 KW Secreted; transmembrane; gene therapy; ss.
 XX
 OS Unidentified.
 XX
 PN WO200078961-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 18-FEB-2000; 2000WO-US004342.

XX 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2001-071395/08.
 DR Secreted and transmembrane proteins and nucleic acids designated PRO,
 PT useful as hybridization probes, in chromosome and gene mapping and gene
 PT therapy.
 XX Claim 2; Fig 171; 787pp; English.
 PS The present invention relates to secreted and transmembrane proteins.
 CC These proteins and the DNA encoding them may be used as hybridization
 CC probes, in chromosome and gene mapping and in the generation of anti-
 CC sense RNA and DNA. They may also be used to generate either
 CC transgenic animals or knockout animals which are in turn useful for
 CC development and screening of therapeutically useful reagents. The nucleic
 CC acids may also be used in gene therapy
 XX
 SQ Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;
 Query Match 26.5%; Score 718.6; DB 4; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 1.4e-205;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
 QY 269 AATGGAGAACAAATGTGCCAGGCTGAATATCTCTACAAAGAAATGTGGAATCCAC 328
 DB 215 ACTTTGAAGCAAAATATTCAGAGCTCAAGCTAACTCAAGAGACTGTCTCTTCAAT 274
 QY 329 AATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACACTTCTCTTGGAT 388
 DB 275 AGCTGATTCCTTTTGGGTTTCATCAGAGAGCTGGATTTTCAAACTCTCTCTAGAT 334
 QY 389 GAGGAACGGAGTAGGCTGTATGTGGAGCAAAAGGATCATATATTTCAATTCGACCTGGTT 448
 DB 335 GAGGAAGAGGCGGCTGCTTGGGAGCCAAAGACCATCTTCTACTCAGTCTGGTT 394
 QY 449 AA---TATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAA 505
 DB 395 GACTTAAACAAAATTTTAAAGATTTTATGGCTGCTGCAAGAGGAGCGGTGGAATTA 454
 QY 506 TCGAAGTGGCTGGAAGACATCTCTGAAAGATGTGCTAAATTTTCAATCAAGTACTTAAG 565
 DB 455 TGTAAATTAGCTTGGGAAAGATGCCAATACAGATGTGCAATTTTATCAGAGTACTTCAG 514
 QY 566 GCATATAATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTTCATCCAATTTGCACC 625
 DB 515 CCTATAACAAAATCCACATATATGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGG 574
 QY 626 TACATTGAAATTTGGACATCATCTCTGAGGACATATTTTTTAAGCTGGAGAACTCAATTTT 585
 DB 575 TATATTGATCTTGGAGCTTACAGGAGGATATTTATTTCAAACTAGACACACATATTTG 634
 QY 686 GAAACGGCGGTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATA 745
 DB 635 GAGTCTGGCAGACTGAATGTCTCTTCGATCTCTCAGCAGCCTTTTGTCTCAGTAATGACA 694

QY 746 GATGGAGAAATTATCTCTGGAACCTGACGCTGATTTTATGGGCGAGACTTTGCTATCTTC 805
 DB 695 GATGAGTACCTCTACTCTGGAACAGACTTTCTGATTTTCTTGGCAAAGACTATGCTACT 754
 QY 806 CGAAGCTCTTGGGC-----ACCACCACCAATCAGACAGACAGCAGCATGATTTCCAGG 856
 DB 755 CGATCCCTTGGGCTTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTAC 814
 QY 857 TGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAAATCTCTGAA 916
 DB 815 TGGCTCAATGGAGCAAAATTTTATTGGAATCTTCTTATACACAGACACCTTACAATCCAGAT 874
 QY 917 GATGACAAAGTATATCTTTTCTTCGTTGAAATGCAATAGTAGGAGACACACTCTGAAA 976
 DB 875 GATGATNAATATATATTTCTTCTTCGTTGAAATCATCTCAAGAGGAGGAGTACCTCCGATAAA 934
 QY 977 GCTACTCAGCTAGAAATAGGTGAGATATGCAAGAAATGACTTTGGAGGGGACAGAAAGTCTG 1036
 DB 935 ACCATCTTCTCGAGTTTGGAGAGTTTGTAGAATGATGTAGGAGGACACAGCGACCTG 994
 QY 1037 GTGAATAAATGGACAAATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAAT 1096
 DB 995 ATAAACAAGTGGAGCACTTTTCTTAAGCCAGACTGATTTGCTCAATCTCTGGAAGTAT 1054
 QY 1097 GGCATTGACACTCATTTTGTAGAACTGAGGATGTATTCTTAATGAATTTTAAAGATCTCT 1156
 DB 1055 GGGGCGAGATATCTTACTTGTAGCTTCAAGATATTTATTTACTCCCCCAAGAGATGAA 1114
 QY 1157 AAAAATCCAGTTGTATATGAGTGTTTTACGACTTCCAGTAAATTTTCAAGGATCAGGC 1216
 DB 1115 AGAAATCTGTAGTATATGAGTCTTTTACTACACAGCTCATCTTCAAGGCTCTGCT 1174
 QY 1217 GTGTGTATGTATAGCATGATGTAGAGAGGTTTCTTGGTCCATATATCCCAAGG 1276
 DB 1175 GTTGTGTGTATAGCATGCTGACATCAGAGCAGTTTTTAATGTTCCATATGCTCATAAG 1234
 QY 1277 GATGACCAACTATCAATGGTGGCTTTTCAAGAGAGTCCCTTATCCAGGCGCAGGA 1336
 DB 1235 GAAAGTGCAGACCATCTGTTGGTGAGTATGATGGGAGAAATTTCTTATCCACGGCTGTG 1294
 QY 1337 ACTTGTCCAGCAAAACATTTG---GTGTTTTGACTCTACAAAGAGCCTTCTCTGATGAT 1393
 DB 1295 ACATGTCCAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
 QY 1394 GTTATAACCTTTTGAAGAGTCAATCCAGCAGTGTCAATCCAGTGTTCCTATGAACAAT 1453
 DB 1355 GTCATCAGTTTCCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCAGTTGCGAGA 1414
 QY 1434 CGCCCAATAGTGTATCAAAACGGATGTAAATTTATCAATTTTACACAAATTTGCTAGACCA 1513
 DB 1415 GGACCAACGTTTCAAGAGAAATCAATGTGATTTACAGACTGACACAGATAGTGTGATCAT 1474
 QY 1514 GTGGATGAGAGAGTGGACAGTATGATGTTTATGTTTATCGGAAACAGATGTTGGGACCGTT 1573
 DB 1475 GTCAATGGAGAGATGGCCAGTACGATGTAATGTTTCTTGGAAACAGACATTTGGAAGTGT 1534
 QY 1574 CTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTGAAGAGGTTTCTGTGGAA 1633
 DB 1535 CTCAAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGGAGTAGTGTCTGGAG 1591
 QY 1634 GAAATGACAGATTTTTCGGGAACCGATGCTATTTTACGCAATGAGGCTTTCCACTAAGCAG 1693
 DB 1592 GAGTTGCGAGATATTTCAAGCACTCATCAATCATCTTTGAAACATGGAATTTGCTCTGAAGCAG 1651
 QY 1694 CAACAATATATATTTGTTTCAACGCTGGGTTTCCAGCTCCCTTACACCGGTGTGAT 1753
 DB 1652 CAACAATTTGATGTTTGGTTTCCGAGATGAGTATGTTTCACTCTCTTGGACAGATGCGAC 1711
 QY 1754 ATTTACGGGAAGCGGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTCTTGGAT 1813
 DB 1712 ACTTATGGGAAGCTTGGCAGACTGTTGCTCTTCCAGAGAGACCTTACTGTCTGCTGGAT 1771
 QY 1814 GGTCTGCAATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCACAGACGACAGATATA 1873

Db 1772 GGAATGCTGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGACGCCAAGATGTA 1831
 Qy 1874 AGAATGGAGACCCACTGACTCACTGTTGAGACTTACACCATGATATCAATCCATGCCAC 1933
 Db 1832 AAATATGGGACCCCAATCAACCCAGTCTGGGACATCGAAGACAGCATTTAGTCATG---AA 1888
 Qy 1934 AGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGATAGTACACATTTTGGAAATGCAGT 1993
 Db 1889 ACTGCTGATGAAGTGATTTTGGCATTTAACTCAACCTTCTGGAATGTATA 1948
 Qy 1994 CCGAAGTCCAGAGACCGCTGTCTATTGGCAATTCAGAGCGCAAAATGAAGAGCGAAA 2053
 Db 1949 CCTAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGTTCAGGGATGAGCATCGA 2008
 Qy 2054 GAAGATCAGATGAGTATCATATCATCAGACAGATCAAGGCCCTTCTGCTAGTGT 2113
 Db 2009 GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAT 2068
 Qy 2114 CTACACAGAAGATTCAAGCAATTAACCTCTGCCATGCGGTGGAAACATGGTTTCATACAA 2173
 Db 2069 TTGCAGAGAAGATTCTGGGATGTATTACTGCAAGCCAGAGACACATTTTCATCCAC 2128
 Qy 2174 ACTCTTTTAAAGTAACCTCGAAGTCAATGACACAGACATTTGGAAGAACTTCTTCAT 2233
 Db 2129 ACCATAGTGAAGTGAATTTGAATGTCAATGAGATGAACAGATGGAATAATCCAGAGG 2188
 Qy 2234 AAAGATGATGATG 2246
 Db 2189 GCAGAGCATGAGG 2201

RESULT 14

AAS46098
 ID AAS46098 standard; cDNA; 3871 BP.

AC AAS46098;

XX 18-DEC-2001 (first entry)

DE Human DNA encoding PRO polypeptide sequence #174.

XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
 KW PCR primer.

XX Homo sapiens.

XX WO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US005601.

XX 02-MAR-2000; 2000WO-US005841.

XX 03-MAR-2000; 2000US-0187202P.

XX 06-MAR-2000; 2000US-0186968P.

XX 14-MAR-2000; 2000US-0189320P.

XX 15-MAR-2000; 2000WO-US006884.

XX 21-MAR-2000; 2000US-0190828P.

XX 21-MAR-2000; 2000US-0191007P.

XX 21-MAR-2000; 2000US-0191048P.

XX 21-MAR-2000; 2000US-0191314P.

XX 28-MAR-2000; 2000US-0192655P.

XX 29-MAR-2000; 2000US-0193032P.

XX 29-MAR-2000; 2000US-0193053P.

XX 30-MAR-2000; 2000WO-US008439.

XX 04-APR-2000; 2000US-0194449P.

XX 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199554P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.

XX (GETH) GENENTECH INC.

PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

DR WPI; 2001-602746/68.

DR P-PSDB; AAU29197.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.

XX Claim 2; Fig 347; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
 CC primers for PRO polypeptides of the invention. The sequences of the
 CC invention can be used to detect the presence of a tumour in a mammal by
 CC comparing the level of expression of a PRO polypeptide in a test sample
 CC of cells from the animal and a control sample of normal cells, whereby a
 CC higher level of expression in the test sample indicates the presence of a
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human
 CC blood, when contacted with it. A specific polypeptide can be used to
 CC stimulate the proliferation or differentiation of chondrocyte cells. The
 CC PRO proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 U; 0 Other;

Query Match 26.5%; Score 718.6; DB 4; Length 3871;

Best Local Similarity 61.9%; Pred. No. 1.4e-205;

Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

Qy 269 AATGGGAAGAACAAATGTGCCAAGGCTGAATATTCCTACAAAGAAATTTGGAATCCAAC 328

Db 215 ACTTTGAAGCAAAATATTCCAAGACTCAAGCTAACCTACAAAGACTTCTGCTTTCAAAAT 274

Qy 329 AATGTGATCACTTTCATGGCTTGGCCCAAGCTCCAGTTATCATACCTTCTTTTGGAT 388

Db 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGACTGGATTTTCAAACTCTTCTCTTAGAT 334

Qy 389 GAGGAACCGAGTAGGCTGTATGTTGGAGCAAGAGTACATATTTTCAATCGACCTGGTT 448

Db 335 GAGGAAGAGCAGGCTGCTCTTGGGAGCCAAAGACACATCTTTCTACTCAGTCTGGTT 394

Qy 449 AA---TATCAAGGATTTTCAAAAGATTTGTGTGGCCAGTATCTTACACCAAGAGATGAA 505

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PR	10-SEP-1998;	98US-0099754P.	
PR	10-SEP-1998;	98US-0099763P.	
PR	10-SEP-1998;	98US-0099812P.	
PR	15-SEP-1998;	98US-0100388P.	
PR	16-SEP-1998;	98US-0100662P.	
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PR	16-SEP-1998;	98US-0101751P.	
PR	16-SEP-1998;	98US-0101933P.	
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PR	18-SEP-1998;	98US-0100849P.	
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PR	18-SEP-1998;	98US-0101068P.	
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PR	23-SEP-1998;	98US-0101477P.	
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PR	24-SEP-1998;	98US-0101739P.	
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PR	01-OCT-1998;	98US-0102687P.	
Query Match 26.5%; Score 718.6; DB 8; Length 3871;			
Best Local Similarity 61.9%; Pred. No. 1.4e-205;			
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;			
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QY	329	AATGTGATCACTTCAATGGCTTGGCCAAAGCTCCAGTTCATATATCATACCTTCTTTGGAT	388
DB	- 275	AGCTGTATTCCTTTTGGGTTTCATCAGAAGGACTGGAATTTCAAACTCTTCTTTAGAT	334
QY	389	GAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCATATTTTCATTCGACCTGTT	448
DB	335	GAGGAAGAGGCGAGGCTGCTCTTGGAGGCCAAAGACCACATCTTTCTACTAGTCTGGTT	394
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DB	455	TGTAATTTAGCTGGGAAGATGCCAATACAGATGTGCAATTTTCATCAGAGTACTTCAG	514
QY	566	GCATATAATCAGACTCACTTGCTGAGCTGTGGAACGGGGGCTTTTCATCAATTTGCAAC	625
DB	515	CCCTATAACAAAACTCACATATATGTGTGGAACCTGGAGCATTTTCATCCAATATGTGG	574
QY	626	TACATTGAATTTGGACATCATCTCTGAGGCAATATTTTAAAGCTGGAGAACTCACATTTT	685
DB	575	TATATTTGATCTTTGGAGTCTACAGAGGAGATATTTATTTCAAACTAGACACATATTTG	634
QY	686	GAAGACGGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAAATA	745
DB	635	GAGTCTGGCAGACTGAAATGTCTTTTCGATCTCTCAGCAGCCTTTTTCAGTAATGACA	694
QY	746	GATGGAGAATTAATCTCTGGAATCGAGCTGATTTTATGGGGCAGACTTTGCTATCTTC	805

DB	695	GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATATGCTCATCTACT	754
QY	806	CGAACTCTTTGGGC-----ACCACCAACCAATCAGACACAGACAGCATGATTCACAG	856
DB	755	CGATCCCTTTGGGCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGACACTAC	814
QY	857	TGGCTCAATGATCCAAAGTTCAATTTAGTGGCCACCTCATCTCAGAGAGTGCATCTCTGAA	916
DB	815	TGGCTCAATGGAGCAAAATTTTATGGAATCTTTCTTCATACCAAGACACCTTACAACTCA	874
QY	917	GATGACAAAGTATATCTTTTCTTCGTGAAATGCAATAGATGGAGAACACTCTCTGAAAA	976
DB	875	GATGATAAATATATATTTCTTTCTGTAATCATCTCAAGAGGAGGAGTACCTTCGATAAA	934
QY	977	GCTACTCAGCTAGATAGGTGAGATATGCAAGATGACTTTTGGAGGGCAGAGAGTCTG	1036
DB	935	ACCATCTTTCTCGAGTTTGAAGAGTTTGTAAAGATGATGTAGGAGGACAAACGACGCTG	994
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QY	1157	AAAAATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGATCAGCC	1216
DB	1115	AGAAATCTGTAGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAGGCTCTGCT	1174
QY	1217	GTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTTCATATGCTCCACAGG	1276
DB	1175	GTTCGTGTATAGCATGCTGCATCAGACGAGCTTTTAAATGGTCCATATGCTCATAAG	1234
QY	1277	GATGACCAACTCATCAATGGGTGCTTATCAAGAGAGTCCCTATCCAGGCCAGGA	1336
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QY	1337	ACTTGTCCAGCAAAACATTTTG---GTGGTTTTGACTCTTACAAAGGACCTTCTCTGATGAT	1393
DB	1295	ACATGTCCAAGCAAAACCTATGACCCACTGATTAGTCCACCCGAGATTTTCCAGATGAT	1354
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DB	1355	GTCAATCAGTTTCATAAAGCGGCACTCTGTGATGTATAGTCCGTATACCCAGTTGCAAGA	1414
QY	1454	CGCCCAATAGTATCAAAACGGATGTAATTAATCAATTTTACAAATTTCTGCTAGACCGA	1513
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QY	1514	GTGGATGCAGAAAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT	1573
DB	1475	GTCAATGCAAGATGGCCAGTACGATGTAATGTTTCTTGGAAACAGACATTTGGAATGTC	1534
QY	1574	CTTAAAGTAGTTTCAATTTCTTAAGAGACTTGGTATGATTTTAAAGAGGTTCCTCTGGAA	1633
DB	1535	CTCAAGTTGTGAGCATTTCAAAGGAAAGTGG---AATATGGAAGAGGAGTAGTCTGGAG	1591
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QY	1694	CAACAACTATATATTTGTTTCAACGGCTGGGTTCGCCAGCTCCCTTTTACACCGGTGTGAT	1753
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QY	1754	ATTTACGGGAAACGCTGTGCTGAGTGTTCGCTCGCCGAGACCTTTATCTGTCTTGGGAT	1813
DB	1712	ACTTATGGGAAAGCTTGGCAGACTGTTGTCTTTGCCAGAGACCCCTACTGTGCTGGGAT	1771
QY	1814	GGTTCGTGATGTTCTGCTGATTTTCCACTGCAAGAGAGCGCAGACGACAGATATA	1873
DB	1772	GGAAATGATGCTCTCGATATGCTCTACTTCTTAAAGAGAGAGCTAGACGCCAAGATGTA	1831

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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 03:13:36 ; Search time 489 Seconds
(without alignments)
9064.772 Million cell updates/sec

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Perfect score: 2709
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2508.4	92.6	2601	US-08-121-713D-53	Sequence 53, Appl
2	2508.4	92.6	2601	US-08-835-268-53	Sequence 53, Appl
3	2508.4	92.6	2601	US-09-060-692-53	Sequence 53, Appl
4	2508.4	92.6	2601	US-08-833-391-53	Sequence 53, Appl
5	2508.4	92.6	2601	US-09-060-610-53	Sequence 53, Appl
6	2508.4	92.6	2601	PCT-US94-10151A-53	Sequence 53, Appl
7	1415.2	52.2	1481	US-08-136-922-1	Sequence 1, Appl
8	596.4	22.0	2898	US-09-308-179B-2	Sequence 2, Appl
9	552.8	20.4	5177	US-09-814-915A-79	Sequence 79, Appl
10	474.8	17.5	2349	US-09-813-290-3	Sequence 3, Appl
11	474.8	17.5	2628	US-09-813-290-1	Sequence 1, Appl
12	473.6	17.5	3568	US-09-813-290-5	Sequence 5, Appl
13	138.8	5.1	229	US-09-513-999C-2555	Sequence 2555, Ap
14	125	4.6	1890	US-09-520-781-29	Sequence 29, Appl
15	125	4.6	2278	US-09-376-594-1002	Sequence 1002, Ap
16	125	4.6	3333	US-09-520-781-5	Sequence 5, Appl
17	125	4.6	3498	US-09-520-781-3	Sequence 3, Appl
18	125	4.6	4280	US-09-774-528-330	Sequence 330, App
19	95.2	3.5	3692	US-09-077-940A-1	Sequence 1, Appl
20	91.2	3.4	300	US-09-513-999C-419	Sequence 419, App
21	90.6	3.3	1923	US-09-653-274-12	Sequence 12, Appl
22	90.6	3.3	1923	US-10-461-791-12	Sequence 12, Appl
23	90.6	3.3	3261	US-09-653-274-5	Sequence 5, Appl
24	90.6	3.3	3261	US-10-461-791-5	Sequence 5, Appl
25	90.6	3.3	3694	US-09-653-274-3	Sequence 3, Appl
26	90.6	3.3	3694	US-10-461-791-3	Sequence 3, Appl
27	84	3.1	2433	US-09-300-958A-24	Sequence 24, Appl

28	83.2	3.1	4157	4	US-08-556-422A-1	Sequence 1, Appl
29	69.8	2.6	2854	1	US-08-121-713D-57	Sequence 57, Appl
30	69.8	2.6	2854	1	US-08-835-268-57	Sequence 57, Appl
31	69.8	2.6	2854	3	US-09-060-692-57	Sequence 57, Appl
32	69.8	2.6	2854	3	US-08-833-391-57	Sequence 57, Appl
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36	68.4	2.5	3432	4	US-09-254-594-4	Sequence 4, Appl
37	63.8	2.4	2283	4	US-09-578-063-18	Sequence 18, Appl
38	63.8	2.4	3104	4	US-09-578-063-17	Sequence 17, Appl
39	60.6	2.2	3524	4	US-09-077-940A-3	Sequence 3, Appl
40	60.2	2.2	2820	4	US-09-854-845-15	Sequence 15, Appl
41	60.2	2.2	2865	4	US-09-854-845-13	Sequence 13, Appl
42	60.2	2.2	3105	4	US-09-854-845-5	Sequence 5, Appl
43	60.2	2.2	3150	4	US-09-854-845-1	Sequence 1, Appl
44	60.2	2.2	3237	4	US-09-854-845-7	Sequence 7, Appl
45	60.2	2.2	3282	4	US-09-854-845-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-121-713D-53
; Sequence 53, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-08-121-713D-53
Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;

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Db	129	AATGTTGGAATCAACAATGTGATCACTTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA	188
QY	373	TACCTTCCTTTTGGATGGAGACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT	432
Db	189	TACCTTCCTTTTGGATGGAGACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT	248
QY	433	TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACAC	492
Db	249	TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACAC	308
QY	493	CAGAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTTAATTCAT	552
Db	309	CAGAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTTAATTCAT	368
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAAGGGGCTTTTCA	612
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QY	673	GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCTTAAGCTGCTGACAGC	732
Db	489	GAACTCACATTTTGAAGACGGCCGTGGGAAGAGTCCATATGACCCTTAAGCTGCTGACAGC	548
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QY	973	AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTGGAGGGCCACAGAAG	1032
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QY	1393	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTATCAATCCAGTGTCTTCTATGAACAA	1452
Db	1209	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTATCAATCCAGTGTCTTCTATGAACAA	1268
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QY	1573	TCCTTAAAGTAGTTCAATTCCTAAGGACATTTGGTATGATTTAGAGAGGTTCTGCTGGA	1632
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QY	1633	AGAAATGACAGTTTTTTCGGGAACCGACTGTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA	1692
Db	1449	AGAAATGACAGTTTTTTCGGGAACCGACTGTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA	1508
QY	1693	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTTCCCTTTTACACCGGTGTGA	1752
Db	1509	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTTCCCTTTTACACCGGTGTGA	1568
QY	1753	TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTGCTTGGGA	1812
Db	1569	TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTGCTTGGGA	1628
QY	1813	TGGTTCTGCTGATTTCTGCTATTTTCCCACTGCAAAAGAGAGCGCAACAGCACAGATAT	1872
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QY	1873	AAGAAATGGAGACCCACTGACTCTGTTTTCAGACTTACACCATGATAATACCATGGGCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCTGTTTTCAGACTTACACCATGATAATACCATGGGCA	1748
QY	1933	CAGCCCTGAAAGAGAGATCATCTATGTTGTTAGAGATAGTAGACATTTTGGAGTGCAG	1992
Db	1749	CAGCCCTGAAAGAGAGATCATCTATGTTGTTAGAGATAGTAGACATTTTGGAGTGCAG	1808
QY	1993	TCCGAAAGTCGAGAGAGCGCTGGTCTATTGGCAATTCAGAGGGCGAAATGAAGCGGAAA	2052
Db	1809	TCCGAAAGTCGAGAGAGCGCTGGTCTATTGGCAATTCAGAGGGCGAAATGAAGCGGAAA	1868
QY	2053	AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	1928
QY	2113	TCTACAAAGAGAGATTCAGGCAATTTACCTCTGCCATGGGTGGAAACATGGGTTTCATACA	2172
Db	1929	TCTACAAAGAGAGATTCAGGCAATTTACCTCTGCCATGGGTGGAAACATGGGTTTCATACA	1988
QY	2173	AACCTCTTAAAGGTAAACCTCGGAAGTCATTGACACAGAGCATTTTGGAGAACTTCTTCA	2232
Db	1989	AACCTCTTAAAGGTAAACCTCGGAAGTCATTGACACAGAGCATTTTGGAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGAGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGATGACACCTAG	2292
Db	2049	TAAAGATGATGAGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGATGACACCTAG	2108
QY	2293	CCAGAGGTCTGGTACAGAGACTTTCATGACCTCATCAACCCCAATCTCAACACCAT	2352
Db	2109	CCAGAGGTCTGGTACAGAGACTTTCATGACCTCATCAACCCCAATCTCAACACCAT	2168

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QY 2353 GGATGAGTTCTGTGAACAAGTTTGGAAAAAGGACCGAAAAACAACGTCGGCAAGGCCAGG 2412
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QY 2413 ACATACCCAGGGAACAGTAACAATGGAAGCACTTACAAAGAAATAAAGAAAGGTAGAAA 2472
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QY 2473 CAGGAGGACCCAGAAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATTACCTCTAGA 2532
Db 2289 CAGGAGGACCCAGAAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATTACCTCTAGA 2348
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Db 2409 GAACTTTTTTCATGGCATTATGTGGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTATAAATTAATCCATGAGTAACCTTCTTAATAGGCTTTTTTTTCC 2702
Db 2469 CCAATTATAAATTAATCCATGAGTAACCTTCTTAATAGGCTTTTTTTTCC 2518

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RESULT 2

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US-08-835-268-53
; Sequence 53, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS

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; LOCATION: 16..2331
US-08-835-268-53
Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 193 CTGAGCATGGGCTGGTAACTAGGATTGTCTGTCTTTTCTGGGAGTATTACTTACAGC 252
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QY 253 AAGACCAACTATCAGAAATGGGAAGCAACAATGTCGCAAGGCTGAAATTTATCTTACAAAGA 312
Db 69 AAGACCAACTATCAGAAATGGGAAGCAACAATGTCGCAAGGCTGAAATTTATCTTACAAAGA 128
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Db 489 GAACTCACATTTTGAAAAACGGCGGTGGGAAGAGTCCATATGACCTTAAAGCTGACAGC 548
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Db 729 TGAAGTACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGGAACACTCTCG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGGTGAGATGCAAGAAATGATCTTTGAGGGGACAGAAAG 1032
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QY 1033 TCTGTGTAATAAATGGACAACATTTCTCAAGCTCGTGTGTTTCTCAGTCCAGGTC 1092
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QY 1093 AAATGGCAATGACACTCAATTTTGTAGTGAATGAGGATGATTTCTTAATGAATCTTTAAAGA 1152
Db 909 AAATGGCAATGACACTCAATTTTGTAGTGAATGAGGATGATTTCTTAATGAATCTTTAAAGA 968
QY 1153 TCCTAAAAATCCAGTTGTATATGAGAGTGTATACGACTTCCAGTAAATTTTCAAGGATC 1212

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Db 969 TCCTAAAAATCCAGTTGTATATGAGAGTTTACGACTTCCAGTAACATTTTCAAGGGATC 1028
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 QY 1273 CAGGATGGACCCAACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTATPCCAGGCC 1332
 Db 1089 CAGGATGGACCCAACTATCAATGGTGTCTTATCAAGGAAGAGTCCCTATPCCAGGCC 1148
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 Db 1149 AGGAATCTGTCCAGCAAAACATTTGGTGGTGTTCGACTCTCAAAAGGACCTTCTGTATGA 1208
 QY 1393 TGTATTAACCTTTGCAAGAGTTCATCCAGCCATGTACAAATCAGTGTTCCTATGAACAA 1452
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 QY 2053 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 2112
 Db 1869 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAG 1928
 QY 2113 TCTCAACAGAGAGGATTCAGGCAATTAATCTCTGCCATCGGTTGGAAACATGGTTTCATACA 2172
 Db 1929 TCTCAACAGAGAGGATTCAGGCAATTAATCTCTGCCATCGGTTGGAAACATGGTTTCATACA 1988
 QY 2173 AACTCTTCTTAAGGTAACCCCTGGAAGTCAATGACACAGAGCAATTTGGAAAGCACTTCTTCA 2232
 Db 1989 AACTCTTCTTAAGGTAACCCCTGGAAGTCAATGACACAGAGCAATTTGGAAAGCACTTCTTCA 2048
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 Db 2049 TAAAGATGATGAGATGGCTCTTAAGACCAAGAAATGTCATATAGCATGACACCTAG 2108

QY 2293 CCAGAAGGTCTGGTACAGAGACTTTCATGAGTCTCATCAACCAACCCCAATCTCAACAGAT 2352
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 Db 2229 ACATACCCCGGACAGTACAAATGGAACACCTTACAGAAATAGAAAGGTAGAAA 2288
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RESULT 3
 US-09-060-692-53
 ; Sequence 53, Application US/09060692
 ; Patent No 5935865
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,692
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 53:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2601 base pairs
 ; TYPE: nucleic acid

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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
US-09-060-692-53

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Query Match      92.6%; Score 2508.4; DB 2; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0;
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Qy	1213	AGCCGTGTGTATGTATAGCATAGATGATGTGAGAGAGGTGTTCCTTGGTCCATATGCCCCA	1272
Db	1029	AGCCGTGTGTATGTATAGCATAGATGATGTGAGAGAGGTGTTCCTTGGTCCATATGCCCCA	1088
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Db	1149	AGGAACCTGTCCAGCAAAAACATTTGGTGGTTTGTACTCTACAAAGACCTTCTCTGATGA	1208
Qy	1393	TGTTATAACTTTGCAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTCTATGAACAA	1452
Db	1209	TGTTATAACTTTGCAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTCTATGAACAA	1268
Qy	1453	TCGCCAAATAGTCATCAAAACGGATGTAAATTTATCAATTTTACACAAATTTGCTGAGACCG	1512
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Qy	1513	AGTGGATGCAGAAGATGGACAGTATGATGTATTATGTTTATCCGAACAGATGTTGGGACCGT	1572
Db	1329	AGTGGATGCAGAAGATGGACAGTATGATGTATTATGTTTATCCGAACAGATGTTGGGACCGT	1388
Qy	1573	TCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTTCTGCTGGA	1632
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Qy	1633	AGAAATCACAGTTTTTCGGGAAACCGACTGTAATTTCCAGCAATGGAGCTTCCCACTAAGCA	1692
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Qy	1693	GCAACAACATATATATTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTA	1752
Db	1509	GCAACAACATATATATTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTA	1568
Qy	1753	TATTTACGGGAAAGCGTGTCTGAGTGTGCTCGCCCGAGACCTTTACTGTGCTTGGGA	1812
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Qy	1813	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAGACGACAAGATAT	1872
Db	1629	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAGACGACAAGATAT	1688
Qy	1873	AAGAAATGGAGACCCACTGACTCACTGTTCCAGACTTACACCATGATTAATCACCATGGCCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCACTGTTCCAGACTTACACCATGATTAATCACCATGGCCA	1748
Qy	1933	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATGATGACACATTTTGGAAATGCAG	1992
Db	1749	CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATGATGACACATTTTGGAAATGCAG	1808
Qy	1993	TCCGAAGTCCAGAGAGCGCTGCTATTTGGCAATTTCCAGAGCGGAATGAAGAGCGGAA	2052
Db	1809	TCCGAAGTCCAGAGAGCGCTGCTATTTGGCAATTTCCAGAGCGGAATGAAGAGCGGAA	1868
Qy	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACCGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACCGTAG	1928
Qy	2113	TCTACACAGAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTTATACA	2172
Db	1929	TCTACACAGAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTTATACA	1988
Qy	2173	AACCTCTTTAAGGTAAACCTTGGAGTTCATTGACACAGGCAATTTGGAAGAACTTCTTCA	2232

Db 1989 AACTCTTCTTAAGGTAAACCTCGAAGTCAATTGACACAGAGCATTTGGGAAGAACTCTTCA 2048
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QY 2353 GGATGAGTCTGTGACAAAGTTTGGAAAGGACCGGAAACCAACCTCGGCAAGGCCAGG 2412
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Db 2409 GAACTTTTTTCATGTCATTTATGTCATTTGATGTTTCAATGGTGGAAATTCAGCTGAGTTCA 2468
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RESULT 4

US-08-833-391-53
; Sequence 53, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Mathes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342

TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
US-08-833-391-53

Query Match 92.6%; Score 2508.4; DB 3; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTCGAGCATGGCTGGTTAACTAGGATTTGCTGCTTTTCTGGGAGATTTACTTTACAGC 252
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Db 69 AAGAGCAAACTATCAGAAATGGGAAGCAAAATGTGCAAGGCTGAAATTTATCTACAAAGA 128
QY 313 AATGTTGGAATCCAACTATGTCATCTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAACTATGTCATCTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
QY 373 TACCTTCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCACAATTT 432
Db 189 TACCTTCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCACAATTT 248
QY 433 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGATCTTTACAC 492
Db 249 TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGATCTTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 368
QY 553 CAAGGTACTTAAGGCATATAATCAGACTCCTGTGACGCTGTGAAACGGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATAATCAGACTCCTGTGACGCTGTGAAACGGGGGCTTTTCA 428
QY 613 TCCAAATTTGCACCTACATTTGAAATTTGACATCATCTGAGGCAATATTTTAAAGCTGA 672
Db 429 TCCAAATTTGCACCTACATTTGAAATTTGACATCATCTGAGGCAATATTTTAAAGCTGA 488
QY 673 GAACTCACAATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTAAAGCTGCTGACAGC 732
Db 489 GAACTCACAATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTAAAGCTGCTGACAGC 548
QY 733 ATCCCTTTTAATAGATGAGAAATTAATCTCTGAAATCTGAGTGAATTTTATGGGGCGAGA 792
Db 549 ATCCCTTTTAATAGATGAGAAATTAATCTCTGAAATCTGAGTGAATTTTATGGGGCGAGA 608
QY 793 CTTTGTCTATCTCCGAACCTTTGGGACACCAACCCCAATCAGGACAGACAGCATGATTC 852
Db 609 CTTTGTCTATCTCCGAACCTTTGGGACACCAACCCCAATCAGGACAGACAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGAGAAACATCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAAATGCAATAGATGAGAAACATCTGG 788
QY 973 AAAAGCTACTCAGCTAGAAATGAGTACATATGCAAGATGACTTTGGAGGGCACAGAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATGAGTACATATGCAAGATGACTTTGGAGGGCACAGAG 848

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2601 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
US-09-060-610-53

Query Match	92.6%	Score	2508.4	DB 3	Length	2601	
Best Local Similarity	100.0%	Pred. No.	0				
Matches	2509	Conservative	0	Mismatches	1	Indels	0
							Gaps 0
QY	193	CTGCAGCATGGCTGGTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGC	252				
DB	9	CTGCAGCATGGCTGGTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGC	68				
QY	253	AGAGCAACTATCAGATGGGAGGAGCAATGTCGCGAGGCTGAAATTCCTACAGAGA	312				
DB	69	AAGAGCAACTATCAGATGGGAGGAGCAATGTCGCGAGGCTGAAATTCCTACAGAGA	128				
QY	313	AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA	372				
DB	129	AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCA	188				
QY	373	TACCTTCCTTTGGATGAGGAAACGAGTAGGCTGATGTTGGAGCAAGGATCACATATT	432				
DB	189	TACCTTCCTTTGGATGAGGAAACGAGTAGGCTGATGTTGGAGCAAGGATCACATATT	248				
QY	433	TTCACTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCAGTATCTTAC	492				
DB	249	TTCACTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCAGTATCTTAC	308				
QY	493	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCGAAAGATGTCCTAAATTCAT	552				
DB	309	CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCGAAAGATGTCCTAAATTCAT	368				
QY	553	CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAACGGGGCTTTTCA	612				
DB	369	CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAACGGGGCTTTTCA	428				
QY	613	TCCAAATTCACCTACATTTGAATGGACATCATCTGAGGACATATTTTAAAGCTGGA	672				
DB	429	TCCAAATTCACCTACATTTGAATGGACATCATCTGAGGACATATTTTAAAGCTGGA	488				
QY	673	GAACTCACATTTTGAACCGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC	732				
DB	489	GAACTCACATTTTGAACCGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGC	548				
QY	733	ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGCGAGA	792				
DB	549	ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGCGAGA	608				
QY	793	CTTTGCTATCTTCGGAATCTTTGGGACCAACCACTCAGGACAGACAGCATGATTC	852				
DB	609	CTTTGCTATCTTCGGAATCTTTGGGACCAACCACTCAGGACAGACAGCATGATTC	668				
QY	853	CAGGTGGCTCAATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCC	912				
DB	669	CAGGTGGCTCAATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCC	728				
QY	913	TGAAGATGACAAAGTATACCTTTTCTCGTGGAAATGCAATAGATGGAGAACACTCTGG	972				
DB	729	TGAAGATGACAAAGTATACCTTTTCTCGTGGAAATGCAATAGATGGAGAACACTCTGG	788				

QY	973	AAAAGCTACTCAGCTAGTAAGTGCAGATATGCAAGATGACTTTTGGAGGSCACAGAG	1032				
DB	789	AAAAGCTACTCAGCTAGTAAGTGCAGATATGCAAGATGACTTTTGGAGGSCACAGAG	848				
QY	1033	TCTGCTGAATAAATGGACAAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTCCAGGTC	1092				
DB	849	TCTGCTGAATAAATGGACAAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTCCAGGTC	908				
QY	1093	AAATGGCATTTGACACTCACTTTTGTATGAATCGCAGATGATTTCTTAATGAACCTTAAAGA	1152				
DB	909	AAATGGCATTTGACACTCACTTTTGTATGAATCGCAGATGATTTCTTAATGAACCTTAAAGA	968				
QY	1153	TCCTAAATCCAGTTGTATATGAGTGTTCACACTTCCAGTACATTTTCAAGGGATC	1212				
DB	969	TCCTAAATCCAGTTGTATATGAGTGTTCACACTTCCAGTACATTTTCAAGGGATC	1028				
QY	1213	AGCCGTGTATGTATAGCATGAGTGTCTGAGAAAGGTTTCTTGGTCCATATGCCCA	1272				
DB	1029	AGCCGTGTATGTATAGCATGAGTGTCTGAGAAAGGTTTCTTGGTCCATATGCCCA	1088				
QY	1273	CAGGATGGAACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGCC	1332				
DB	1089	CAGGATGGAACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGCC	1148				
QY	1333	AGGAACCTTGTCCAGCAAAACATTTTGGTGGTTTTCACCTCAAAAGGACCTTCTCTGATGA	1392				
DB	1149	AGGAACCTTGTCCAGCAAAACATTTTGGTGGTTTTCACCTCAAAAGGACCTTCTCTGATGA	1208				
QY	1393	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCAGTGTCTTCTATGAACAA	1452				
DB	1209	TGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCAGTGTCTTCTATGAACAA	1268				
QY	1453	TGCCCCAATAGTGTCAAAAACGATGTAAATTTCAATTTACAAATTTGCTGTAGACCG	1512				
DB	1269	TGCCCCAATAGTGTCAAAAACGATGTAAATTTCAATTTTACAAATTTGCTGTAGACCG	1328				
QY	1513	AGTGATGCAGAAGATGACAGATGATGTATGTATTTATCGGAAACAGATTTGGGACCGT	1572				
DB	1329	AGTGATGCAGAAGATGACAGATGATGTATGTATTTATCGGAAACAGATTTGGGACCGT	1388				
QY	1573	TCTTAAAGTAGTTCCTCAATTTCTAAGGAGACTTTGGTATGATTTTGAAGAGGTTCTCTGGA	1632				
DB	1389	TCTTAAAGTAGTTCCTCAATTTCTAAGGAGACTTTGGTATGATTTTGAAGAGGTTCTCTGGA	1448				
QY	1633	AGAAATGACAGTTCCTCGGAAACCACTGCTATTTTTCAGCAATGGAGCTTCCACTAAGCA	1692				
DB	1449	AGAAATGACAGTTCCTCGGAAACCACTGCTATTTTTCAGCAATGGAGCTTCCACTAAGCA	1508				
QY	1693	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACGGTGTGA	1752				
DB	1509	GCAACAACTATATATTTGGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACGGTGTGA	1568				
QY	1753	TATTTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTTGTGCTGGGA	1812				
DB	1569	TATTTTACGGGAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTTGTGCTGGGA	1628				
QY	1813	TGGTTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGAGCGACAGATAT	1872				
DB	1629	TGGTTCTGCTATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGAGCGACAGATAT	1688				
QY	1873	AAGAAATGGAGACCACTGACTGCTTTCAGACTTACACCATGATTAATCACCATGGCCA	1932				
DB	1689	AAGAAATGGAGACCACTGACTGCTTTCAGACTTACACCATGATTAATCACCATGGCCA	1748				
QY	1933	CAGCCCTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCAATTTTGGAAATGCAG	1992				
DB	1749	CAGCCCTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCAATTTTGGAAATGCAG	1808				
QY	1993	TCCGAGTCCGAGAGAGCGCTGCTATTTGGCAATTCAGAGCGCAAAATGAGAGCGAAA	2052				
DB	1809	TCCGAGTCCGAGAGAGCGCTGCTATTTGGCAATTCAGAGCGCAAAATGAGAGCGAAA	1868				

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QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG 1928
QY 2113 TCTACAAACAAGAGATTGAGCAATACCTCTGCGCATGCGGTGGAAACATGGGTTTATACA 2172
Db 1929 TCTACAAACAAGAGATTGAGCAATACCTCTGCGCATGCGGTGGAAACATGGGTTTATACA 1988
QY 2173 AACTCTTTTAAGGTAACCTCGAAGTCAATGACACAGAGCAATTTGGAGAACTTTTCA 2232
Db 1989 AACTCTTTTAAGGTAACCTCGAAGTCAATGACACAGAGCAATTTGGAGAACTTTTCA 2048
QY 2233 TAAAGATGATGATGAGTGGCTTCAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGTGGCTTCAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
QY 2293 CCAGAAAGGTTCTGTCAGAGACTTCAATGAGCTCAATCAACACCCCAATCTCAACAGAT 2352
Db 2109 CCAGAAAGGTTCTGTCAGAGACTTCAATGAGCTCAATCAACACCCCAATCTCAACAGAT 2168
QY 2353 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAACACGTCGGCAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTGAACAAAGTTTGGAAAGGGAACCAACACGTCGGCAAGGCCAGG 2228
QY 2413 ACATACCCCAAGGACAGTAAACAAATGGAAGCACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCAAGGACAGTAAACAAATGGAAGCACTTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATACCTTAGA 2532
Db 2289 CAGGAGGACCCAGCAATTTGAGAGGACCCAGGAGTGTCTGAGCTGCAATACCTTAGA 2348
QY 2533 AACCTCAACAAAGTAAAGTCTGCTAGCAATTAACCTGGAAACCAAAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTAAAGTCTGCTAGCAATTAACCTGGAAACCAAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2652
Db 2409 GAACTTTTTCATGTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2468
QY 2653 CAAATTAATAATTAATCATCAGTAACTTTCTTAATAGGCTTTTTCCTCC 2702
Db 2469 CCAATTAATAATTAATCATCAGTAACTTTCTTAATAGGCTTTTTCCTCC 2518

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RESULT 6

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PCT-US94-10151A-53
; Sequence 53, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR HOEBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:

```

```

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16...2331
; PCT-US94-10151A-53

Query Match 92.6%; Score 2508.4; DB 5; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGACGATGGGCTGGTTAACTAGGATTTGTCCTCTTTCTGGGAGTATTAATTCTTACAGC 252
Db 9 CTGACGATGGGCTGGTTAACTAGGATTTGTCCTCTTTCTGGGAGTATTAATTCTTACAGC 68
QY 253 AAGACCAACTATCAGAAATGGGAACAACAATGTGCCAAGGCTGAAATATCTCTACAAAGA 312
Db 69 AAGACCAACTATCAGAAATGGGAACAACAATGTGCCAAGGCTGAAATATCTCTACAAAGA 128
QY 313 AATGTTGGAATCCCAACAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCA 372
Db 129 AATGTTGGAATCCCAACAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCA 188
QY 373 TACCTTCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 432
Db 189 TACCTTCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCAATATT 248
QY 433 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 492
Db 249 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTTGGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAAT 368
QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGTAACGCGGCTGTAACGCGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTGTGTAACGCGGCTGTAACGCGGCTTTTCA 428
QY 613 TCCAAATTTGCACTTACATTTGAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGCACTTACATTTGAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAACTCACAATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 732
Db 489 GAACTCACAATTTTGAACCGCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548
QY 733 ATCCCTTTTAATAGATGAGAAATATATCTCTGGAACCTGACGCTGATTTTATGGGGGAGGA 792
Db 549 ATCCCTTTTAATAGATGAGAAATATATCTCTGGAACCTGACGCTGATTTTATGGGGGAGGA 608
QY 793 CTTTGTCTATCTTCGAACTCTTGGGACACCAACCCCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTTCGAACTCTTGGGACACCAACCCCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCTAAAGTTCATTTAGTGGCCCACTCTCTCAGAGAGTGAACAATCC 912
Db 669 CAGGTGGCTCAATGATCCTAAAGTTCATTTAGTGGCCCACTCTCTCAGAGAGTGAACAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAGAACACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAGAACACTCTGG 788
QY 973 AAAGCTACTCAGCTAGAAATAGTTCAGATATGCAAGATGACTTTGGAGGACAGAG 1032

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789	AAAAGCTACTCTCACCGCTAGAAATAGGTGAGATATGCAAGAAATGACTTTTGGAGGGGCACAGAAAG	848
1033	TCTGCTGAATAAAATGAGCAACATTTCCCTCAAAGCTCGCTGATTTTGCTCAGTGCACGAGTCC	1092
849	TCTGCTGAAATAAATGGACACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCACGAGTCC	908
1093	AAATGGCAATTGACACTCATTTTGAATGAACATGCGAGGATGTATTCTTAATGAACATTTTAAAGA	1152
909	AAATGGCAATTGACACTCATTTTGAATGAACATGCGAGGATGTATTCTTAATGAACATTTTAAAGA	968
1153	TCCTAAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC	1212
969	TCCTAAAAATCCAGTTGTATATGAGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATC	1028
1213	AGCCGTGTGTATGTATAGCAATGAGTGTGAGAGGGTGTTCCTTCGTCCATATGCCCA	1272
1029	AGCCGTGTGTATGTATAGCAATGAGTGTGAGAGGGTGTTCCTTCGTCCATATGCCCA	1088
1273	CAGGGATGGACCCAACTATCAAATGGGTGCCCTTATCAAGAGAGAGTCCCTTATCCACGGCC	1332
1089	CAGGGATGGACCCAACTATCAAATGGGTGCCCTTATCAAGAGAGAGTCCCTTATCCACGGCC	1148
1333	AGGAACTTGTCCAGCAAAAACATTTGTGTGGTTTGTACTCTAAGAGACCTTCTCTGATGA	1392
1149	AGGAACTTGTCCAGCAAAAACATTTGTGTGGTTTGTACTCTAAGAGACCTTCTCTGATGA	1208
1393	TGTTATAACCTTTGCAAGAGAGTCAATCAGAGAGTGTGAGAGGGTGTTCCTTCATGAACAA	1452
1209	TGTTATAACCTTTGCAAGAGAGTCAATCAGAGAGTGTGAGAGGGTGTTCCTTCATGAACAA	1268
1453	TCGCCCAATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAATTTGCTGTAGACCG	1512
1269	TCGCCCAATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAATTTGCTGTAGACCG	1328
1513	AGTGGATGCGAAGATGGACGATGATGTATGTTTTATCGGAAACAGATGTTGGGACCGT	1572
1329	AGTGGATGCGAAGATGGACGATGATGTATGTTTTATCGGAAACAGATGTTGGGACCGT	1388
1573	TCCTTAAAGTAGTTTCAATTCCTTAGGAGACTTGGTATGATTTAGAGAGAGTCTGCTGGA	1632
1389	TCCTTAAAGTAGTTTCAATTCCTTAGGAGACTTGGTATGATTTAGAGAGAGTCTGCTGGA	1448
1633	AGAAATGACAGTTTTTTCGGGAAACCGACTGCTATTTACAGCAATGGAGCTTTCCACTAAGCA	1692
1449	AGAAATGACAGTTTTTTCGGGAAACCGACTGCTATTTACAGCAATGGAGCTTTCCACTAAGCA	1508
1693	GCAACAACTATATATGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACGGGTGTGA	1752
1509	GCAACAACTATATATGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACGGGTGTGA	1568
1753	TATTTACGGGAAAGCGTCTGAGTGTTCCTTCGCCCGGAGACCTTACTGTCTTGGGA	1812
1569	TATTTACGGGAAAGCGTGTGAGTGTTCCTTCGCCCGGAGACCTTACTGTCTTGGGA	1628
1813	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAAAGATAT	1872
1629	TGGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCACAAAGATAT	1688
1873	AAGAAATGGAGACCACTGACTCATCTGTTTACAGACTTACCAATGATTAATCACCATGGCCA	1932
1689	AAGAAATGGAGACCACTGACTCATCTGTTTACAGACTTACCAATGATTAATCACCATGGCCA	1748
1933	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGAAATGCAG	1992
1749	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGAAATGCAG	1808
1993	TCCGAACTGCGAGAGACCGTGGTCTATTTCGCAATTCACAGGCGAAATCAAGAGCGAAA	2052
1809	TCCGAACTGCGAGAGACCGTGGTCTATTTCGCAATTCACAGGCGAAATCAAGAGCGAAA	1868
2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGTCAGTAG	2112
1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGTCAGTAG	1928

QY	2113	TCTACAA	CAGAGG	ATTACGG	CAATTA	CTCTG	CCATG	CGGTG	GAACAT	GGGTTC	ATACA	2172
DB	1929	TCTACAA	CAGAGG	ATTACGG	CAATTA	CTCTG	CCATG	CGGTG	GAACAT	GGGTTC	ATACA	1988
QY	2173	AACCTCT	TTCTTA	AGGTAA	CCCTG	GAGTCA	TTTGA	CACAG	AGCAT	TTTGG	AGAACTT	CTTCA
DB	1989	AACCTCT	TTCTTA	AGGTAA	CCCTG	GAGTCA	TTTGA	CACAG	AGCAT	TTTGG	AGAACTT	CTTCA
QY	2233	TAAAGAT	GATGAT	GGAGAT	GGCTCT	TAA	GACCA	AGAAAT	GTC	CAATAG	CATGAC	ACCTAG
DB	2049	TAAAGAT	GATGAT	GGAGAT	GGCTCT	TAA	GACCA	AGAAAT	GTC	CAATAG	CATGAC	ACCTAG
QY	2293	CCAGAAG	GTCTGG	TACAG	AGACTT	CA	TG	CAGCTC	ATCA	ACCC	CAATCT	CAACACGAT
DB	2109	CCAGAAG	GTCTGG	TACAG	AGACTT	CA	TG	CAGCTC	ATCA	ACCC	CAATCT	CAACACGAT
QY	2353	GGATGAG	TTCTGT	GACAA	CAAGTT	TTG	GA	AAAGG	ACCG	GAAC	CAACGTC	GGCAAAAGGCCAGG
DB	2169	GGATGAG	TTCTGT	GACAA	CAAGTT	TTG	GA	AAAGG	ACCG	GAAC	CAACGTC	GGCAAAAGGCCAGG
QY	2413	ACATAC	CCCCAGG	GAACAG	TAA	CAAA	TG	GGAAG	CACTT	AC	AGAAAA	TAAAGAAAGGTAGAAA
DB	2229	ACATAC	CCCCAGG	GAACAG	TAA	CAAA	TG	GGAAG	CACTT	AC	AGAAAA	TAAAGAAAGGTAGAAA
QY	2473	CAGGAG	ACCCAC	GAA	TTT	TG	AGAGG	GCAC	CC	AGGAGT	GTCTG	AGCTTCA
DB	2289	CAGGAG	ACCCAC	GAA	TTT	TG	AGAGG	GCAC	CC	AGGAGT	GTCTG	AGCTTCA
QY	2533	AACCTG	AAAA	CAAG	TAG	AACTT	CG	CTAG	ACAA	TAA	CTG	GNA
DB	2349	AACCTG	AAAA	CAAG	TAG	AACTT	CG	CTAG	ACAA	TAA	CTG	GNA
QY	2593	GAAC	TTTTTT	CATG	GGCA	TAT	GTG	GA	TGTT	TACA	TGGT	GGG
DB	2409	GAAC	TTTTTT	CATG	GGCA	TAT	GTG	GA	TGTT	TACA	TGGT	GGG
QY	2653	CCAATTA	ATAA	TAAAT	PCC	ATG	AGTAA	CTT	TC	TAAT	AGG	CTTTTTTTTCC
DB	2469	CCAATTA	ATAA	TAAAT	PCC	ATG	AGTAA	CTT	TC	TAAT	AGG	CTTTTTTTTCC

RESULT 7

US-08-136-922-1
; Sequence 1, Application US/08136922
; Patent No. 5416197
; GENERAL INFORMATION:
; APPLICANT: Raper, Jonathan A.
; APPLICANT: Luo, Yuling
; TITLE OF INVENTION: Compositions Which Regulate Neural
; TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: NO. 5416197ris
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/136,922
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: UPN-1428

Query Match		22.0%;	Score 596.4;	DB 3;	Length 2898;
Best Local Similarity		56.3%;	Pred. No. 2.4e-176;		
Matches 1229;		Conservative	0;	Mismatches 931;	Indels 24; Gaps 5;
QY	223	CTGTCTTTCTGGGAGTATTACTTACAGCAAGAGCAAACTATCAGAATGGGAAGAACAA	282		
DB	396	CTTGTCTCTGGGTCACTCTGGAACCTCTGGACCCCGAGTCACTCGCGAACCCCTC	455		
QY	283	TGTGCCAAGCTGAATATCTTACCAAGAAATGTTGGAATCCAAATGTGATCACTTT	342		
DB	456	CTACCCCAAGGCTACGCTGTACATAAAGAACTTTTGGAACTGAATAGGACTTTCAATATT	515		
QY	343	CAATGGCTTGGCAACAGCTCCAGTTATCATACCTTCTCTTTTGGATGAGAACGGAGTAG	402		
DB	516	TCAAAGCCCCCTTGGATTTCTTGATCTCCATACAAATGCTGCTGGATGAGTATCAAGACG	575		
QY	403	GCTGTATGTTGGAGCAAGGATACATATTTTCATTCGACCTGGTTAATATCA---AGGA	459		
DB	576	GCTCTTTTGGGAGGCAGAGACCTTGTCTATTCCCTGAACTTTGGAAACGAGTCAGTGA	635		
QY	460	TTTTCAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGCTGG	519		
DB	636	CTACAGAGAGATATATGCGCCGAGCACAGCAGTAAAGGTAGAAGATGCATAATGAAAGG	695		
QY	520	AAAGACATCTCTGAAAGAAATGTCTAAATTTTCATCAAGGTACTTAAAGGCATATAATCAGAC	579		
DB	696	AAAGAA---CGCAATAGTGTGCCAATTTATATCCGGTTTTCATCTACTACACAGGAC	752		
QY	580	TCATTTGACGCTGTGGAAACGGGGCTTTTCATCCAAATTTGCACTCATATTTGAATTTGG	639		
DB	753	ACACCTTCTGACCTGTCTACTGAGCTTTTGTATCCACACTGTGCTTTCATCAGAGTCGG	812		
QY	640	ACATCATCTGAGGCAATATTTTAAAGCTGAGAACTCACATTTTGAAGCGGCTGG	699		
DB	813	GCACCAATTCAGAGAACCCCTGTTTTCACCTGGAGTCACACAGATCTGAGAGAGGAAGGG	872		
QY	700	GAAAGATCCATATGACCCCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGAGAAATATA	759		
DB	873	CAGATGTCTTTTGGACCCCACTCTCTCTTTGTGTCACGCTAGTTGGGAATGACTGTT	932		
QY	760	CTCTGGAATCGAGCTGATTTTATGGGGGAGACTTTTGCTATCTTTCCGAACCTTTGGGCA	819		
DB	933	TGCTGGAATCTACAGTGAATTTGGGGCAGAGACTCGGCGATCTTCCGACAGCATGGGAA	992		
QY	820	CCACCACCAATCAGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTGAT	879		
DB	993	GTTAGGCCATATTCGCACTGACATGACGATGAGCGGCTCTCTGAAAGAACCAAAATTTGT	1052		
QY	880	TAGTGCCCACTCTCAGAGAGTGACAAATCCTGAAGATGACAAAGTATATCTTTTCTT	939		
DB	1053	AGGTTTCATATATGATTCCTGTATAACGAGACCGAGATGACAAACAAATGTACTTTTCTT	1112		
QY	940	CCGTGAAATGCAATAGATGGAGAACACTCTCTGAAAGACTCTACGCTAGAAATAGGTCA	999		
DB	1113	TACTGAGAAGGGCTGGAGGGCGAGAACAAACGCCACACAGATCTACACCCGAGTGGGCG	1172		
QY	1000	GATATGCAAGATGATTTTGGAGGCAAGAGTCTGGTGAATAAATGGACAACTTCT	1059		
DB	1173	GCTGTGCGTGAATGACATGGGAGGACAGAAATCTCTGTTGAACAAGTGGAGCACTTTCT	1232		
QY	1060	CAAAGCTGCTGTGATTTGCTCAGTGCCAGGTCCAAATGGCAATGACACTCATTTTGTATGA	1119		
DB	1233	TAAAGCGGCTGGTTTGTCTCAGTCCGGGAATGAATGGAATCGACACATCTTTGACGA	1292		
QY	1120	ACTCAGAGATGATTTCTTAATGAACTTTTAAAGATCCTTAAATCCAGTTGTATATGAGT	1179		
DB	1293	ACTAGAGATGTTTCTTACTCCGCCAGAGATCTTAAGATCCAGTGAATATTTGGACT	1352		
QY	1180	GTTTACGACTTCCAGTAAATTTTCAAGGATCAGCGGTGTGTATGTATAGCATGATGA	1239		
DB	1353	GTTTAAATCTACAGCAATATATTTAGAGGCCATGCTGTATGTGTATCATATGTCAAG	1412		

QY	1240	TGTGAGAAAGGTGTTCTTGTGTCATATGCCCACAGAGGATGACCCAACTATCAATGGGT	1299
DB	1413	TATCGGGAAGCTTTAATGCCCCATATGCTCATAAAGAGCCCTGAATACCACTGGTC	1472
QY	1300	GCCTTATCAAGAGAGTCCCTTATCCAGGGCAGGAACTTGTCCAGCAAAACATTTGG	1359
DB	1473	ACTATATGAAGGAAAGTCCCTACTCCCAAGGCTGGTTCTGTGCGCAGCAAGATAACGG	1532
QY	1360	TGG---TTTTGACTCTACAAAAGGCTTCTGTATGATGTTATAAACCCTTTGCAAGAAGTCA	1416
DB	1533	AGGCAAGTATGGAACCAACAAAGATTACCCGATGACGCCATCCGGTTCGCAAGATGCA	1592
QY	1417	TCCAGCCATGACAAATCCAGTGTTCCTATGAAACAAATCGCCCAATAGTATGATCAAAACGGA	1476
DB	1593	TCCTCTATGATCAGCCCATAAAACCTGTTTCATAAAAAACCAATACTGGTAAAAACAGA	1652
QY	1477	TGTAATATCAATTTTACAAAATGTCGTAGACCGAGTGGATGAGTGGAGATGGACAGTA	1536
DB	1653	TGAAAAATACAACTGAGGCAACTTGGCGTGGATCGGGTGGAAAGCGGAGGATGGCCAGTA	1712
QY	1537	TGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAAAGTAGTTTCAATTTCTTAA	1596
DB	1713	TGACGCTTTATTTATTTGGGACAGACACAGGAATTTGCTGAAAGTAATCAACAATTTACAA	1772
QY	1597	GGAGACTTGGTATGATTTTAGAAGAGGTTCTGCTGGAAGAAATGACAGATTTTTCGGGAACC	1656
DB	1773	CCAAAGAACAGATGGATGGAGGAAGTCAATCTTAGAGGAACCTTCAATATTTCAAGGATCC	1832
QY	1657	GACTGCTATTTACGAATGGAGCTTTCCATTAAGCAGCAACAACTATATATTTGGTTCAAC	1716
DB	1833	AGCCCTATCATTTCTATGSAATTTCTTCAAGAGACACACAGCTTTTACATTTGGATCAGC	1892
QY	1717	GGCTGGGCTGCCAGCTCCCTTTTACACGGGTGATATTTACGGGAAAGCGTGTCTGA	1776
DB	1893	CTGCTGTGGACAAAGTCAGATTCATCCATCACTGCAATGATGATGCAAGTCTTTGCTGA	1952
QY	1777	GTGTGCTCCGCCGAGACCCCTTACTGTGCTTGGAGTGGTTCTGATGTTCTCGCTATTTT	1836
DB	1953	CTGCTGCTGCTCGAGACCCGTAATGCTGCTGGGATGGCATATCTGCTCCAGGTACTA	2012
QY	1837	TCCAC-----TGCAAGAGAGCACAAGACGACAGCAAGATATAAGAAATGGAGACCC	1887
DB	2013	CCCAACAGGTGCACACGCAAGAGAGGTTCCGACGAGGACGTTCCGCGCATGGCAACGC	2072
QY	1888	ACTGACTCACTGTTTACAGACTTACCAATGATAATCACCATGCGCCACAGCCCTGGAAGAG	1947
DB	2073	CGCCCAACAGTCTTTTGGACAGCAATTTTGGAGACCGGTTGGACAGACTGAAGAGAG	2132
QY	1948	AATCATCTATGCTGTAGAGAAATAGTAGCACATTTTGGAAATGCAAGTCCGAAAGTCCAGAG	2007
DB	2133	GCTGGCTTATGGCATAGAGAGCAACAGTACTCTGTTGGAATGCAACCCCGCATCACTACA	2192
QY	2008	AGCGTGTCTATTTGGCAATTTCCAGAGCGGAATGGAAGCGGAAGAGAGATCAGAGT	2067
DB	2193	AGCAAAAGTCTATGTTTGTACAGAGGGAACGCGACGTAAAGAAAGAGAGGTGAAGAC	2252
QY	2068	GGATCATCATATCATCAGACAGATCAAGGCTTCTGCTAGCTAGTCTACAAACAGAGGA	2127
DB	2253	GGATGACAGATTTGATGAGATGGACTTGGGCTTGTCTCTCTCAGAGTACCGCAAGTACA	2312
QY	2128	TTGAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTTCATACAACTCTTTCTTAAGGT	2187
DB	2313	TGAGGGACCTATTTTGGCAGACAGTAGAACAACATTTTGTCCATCTGTGCGTAAAT	2372
QY	2188	AACCTGGAAGTCTTGGACAGACATTTTGGAGAACTTCTTCAATAAGATGATGATG-	2246
DB	2373	CACCTTGAAGTGTGCGAAGAGCATAAAGTGGAGGCGATGTTTCAATAGGACCATGAAGA	2432
QY	2247	-----GAGATGGCTCTAAGACCAAAAGAAATGTCCAATAGCATGACACCTAGCCAGAGGT	2301
DB	2433	GGAAAGACATCAAGATGCGCTCCCTTAAAGCGGTATGTCTCAGGGGACAAAACC	2492
QY	2302	CTGGTACAGAGACTTTCATGCACTCATCAACCCCAATCTCAACACGATGGATGAGTT	2361

Db	2493	GTGGTACAAGGAATCTTGAGCTGATGGCTACAGCAACTTCCAGAGAGTGGAGAATA	2552
Qy	2362	CTGTGAACAAGTTTGGAAAAGGGA	2385
Db	2553	CTGGGAAGAGTGTGGTACAGA	2576
RESULT 9			
US-09-814-915A-79			
; Sequence 79, Application US/09814915A			
; Patent No. 6750015			
; GENERAL INFORMATION:			
; APPLICANT: Horwitz, Kathryn			
; APPLICANT: Richer, Jennifer			
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat			
; TITLE OF INVENTION: Theteto			
; FILE REFERENCE: 2848-39			
; CURRENT APPLICATION NUMBER: US/09/814,915A			
; CURRENT FILING DATE: 2002-03-21			
; PRIOR APPLICATION NUMBER: 60/214,870			
; PRIOR FILING DATE: 2000-06-28			
; NUMBER OF SEQ ID NOS: 108			
; SOFTWARE: Patentin version 3.1			
; SEQ ID NO 79			
; LENGTH: 5177			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-814-915A-79			
Query Match 20.4%; Score 552.8; DB 4; Length 5177;			
Best Local Similarity 57.5%; Pred. No. 1.9e-162;			
Matches 1115; Conservative 0; Mismatches 802; Indels 21; Gaps 6;			
Qy	288	CAAGGCTGAATATCTACAGAAGATCTTGGATCCCAATGTGATCACTTTCAATG	347
Db	642	CAAGAGTTTATTAACTTTGATGAATCTCGAAGAACCAAGACCTCTGAATACCTCAGCC	701
Qy	348	GCTTGGCCCAAGCTCCAGTTATCATACCTTCTTTGGATGAGGAACGGAGTAGGCTGT	407
Db	702	TTTCCACCATCTTTAGACTACAGGATTTTATTATGATGAAGATCAGGACCGGATAT	761
Qy	408	ATGTTGGAGCAAGGATCATATTTTTCATTTGACCTGTTTAAATCA---AGGATTTTC	464
Db	762	ATGTGGGAAGCAAGATCACTTCTTCCCTGAATTAATTAACAATATAAGTCAAGAAGCTT	821
Qy	465	AAAAGATTGTGGCCAGTCTTTACACCAAGAGATGAATGCAAGTGGCTGGAAAG	524
Db	822	TGAGTGTCTTGTGGCCAGCATCTACAATCAAAGTTGAAGAAATGCAAAATGGCTGGCAAG	881
Qy	525	ACATCTGAAAGATGTGCTAATTTTCATCAAGTACTTAAGGCATATAATCAGACTCACT	584
Db	882	ATCCACACACGGCTGTGGGAATTTGTCCGTGTAATTCAGACTTTCATTCGCACATTT	941
Qy	585	TGTACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACTTACATTTGAAATTTGGACATC	644
Db	942	TGTATGCTGTGGAGTGGGGCTTTTCAGTCTCTGTCTACTTACTTGAACAGAGGAGGA	1001
Qy	645	ATCCTGAGGACATATTTTAAAGCTGGAGATCTACATTTTGAAGACGGCTGGGAAGA	704
Db	1002	GATCAGAGACCAAGTTTTCATGATTTG---ACTCCAAGTGTGAATCTGGAAAAGGACGCT	1058
Qy	705	GTCCATATACCTTACCTGCTGACAGCATCCCTTTTAAATAGATGGAGAAATTATCTCTG	764
Db	1059	GCTCTTTCAACCCCAAGTGAACACGGTGTCTGTTATGATCAATGAGGAGCTTTTCTCTG	1118
Qy	765	GAACTGACGCTGATTTTATGGGCGGAGACTTTTGCTATCTTCCGAATCTTGGGCCACC	824
Db	1119	GAAATGATATAGATTTCATGGGACAGATGCTGCTATTTTTCGAAGTTTAAACCAAGAGGA	1178
Qy	825	ACCAATCAGGACAGAGCAGATGATTCAGGTGGCTCAATGATCCAAAGTTTCATTTAGT	884
Db	1179	ATGCGGTCAAGACTGATCAACATAATTTCCAAATGGCTAAGTGAACCTATGTTTGTAGATG	1238

Qy	885	CCCACCTCATCTCAGAGAGTGCAATCTGTAAGATGACAAAGTATATCTTTTCTTCCGTG	944
Db	1239	CACATGTATCCAGATGGTACTGATCCAAATGATCTAAGGTACTTCTTCTTCAAAG	1298
Qy	945	AAAATGCAATAGATGGAGAACACTCTGGAAAGACTACTCACCTAGATAGTGCAGATAT	1004
Db	1299	AAAAAATGACTGACATTAACAGGACGACGAATTCATTCATGATGCTCGAATAT	1358
Qy	1005	GCAAGAATGACTTTTGGAGGGCAAGAAAGTCTGGTGAATAAATGGAACAACTTCTCAAAG	1064
Db	1359	GTCTTAATGACACTGGTGGACTGGCTGCTGTCACACAGTGGACCACTTTCTTAAAGG	1418
Qy	1065	CTCGCTGATTTGCTCAGTGCAGGTCGCAATGGAATGACACTCAATTTTGTATGAACTGC	1124
Db	1419	CGAGGCTGTGTGCTCGGTAAACAGATGAAGACGGCCGCAACACACACTTTGTATGAATAG	1478
Qy	1125	AGGATGTTTCTTAATGAACCTTTAAAGATCCTTAAATCCACTGTATATGAGTGTGTTA	1184
Db	1479	AGGATGTTTCTGCTGGAACCTGATAACCCGAGGACAACTAGTGTATGCAATTTTAA	1538
Qy	1185	CGACTTCCAGTAAACATTTTCAAGGATCAGCCGCTGTATGTATAGCATGATGATGA	1244
Db	1539	CAACATCAAGCTCAGTTTCAAGAGTCAAGCCGCTGTGTGTATCATTTATCTGATATAC	1598
Qy	1245	GAAAGGTGTTCTGTCATATGCCACAGGATGGACCCCACTATCAATGGTGGCTTT	1304
Db	1599	AGACTGTGTTTAAATGGGCTTTTGGCCACAAAGAGGGCCCAATCATCAGCTGATTTCT	1658
Qy	1305	ATCAGGAAGAGTCCCTTATCCAGCCGAGGAAGTGTGTCAGCAAAACATTT---GGTG	1361
Db	1659	ATCAGGCGAGAAATTCATATCTCTCCCTCGGAACCTTGTCCAGGAGGAGCATTTACAC	1718
Qy	1362	GTTTTGAAGTCTCAAAAGGACCTTCTGTATGATGTTTATTAACCTTTTGCAGAAAGTCA	1421
Db	1719	ATATCGGAACCAAGAGGTTCCAGATGATGTTGTCACTTTTATTCGGAACCATCTTC	1778
Qy	1422	CCATGTACAATCCAGTGTTCCTATGAACAATCGCCCAATAGTGTATCAAAACGGATGTA	1481
Db	1779	TCATGTACAATTCATCTACCCAAATCCCAAAAGGCTTTGATTTGTTGTCGACCTG	1838
Qy	1482	ATTATCAATTTACACAATTTGCTAGACCGAGTGGATGCAAGATGACAGATGATGATG	1541
Db	1839	ACTACAAGTACACAAGATAGCTGTGGATCGAGTGAACCTCTGATGGGAGATACCTTG	1898
Qy	1542	TTATGTTTATCGGAACAGATGTGGACCGTTCTTAAAGTAGTGTTCATTTCTCTAAGGAG	1601
Db	1899	TCCTGTTTCTCGGAACAGATCGGGGTACTGTGCAAAAGTGGTGTGTTCTTCTTACTA	1958
Qy	1602	CTTGTGATGATTTAGAAGAGTTCGTGTGGAAGAAATGACAGTGTTCGGGAACCGACTG	1661
Db	1959	---ACTGTGTAGTGGCGAGCTCAATTCGGAGGAGCTGGAAAGTCTTTAAGAAATCATG	2015
Qy	1662	CTATTTTACAGATGAGCTTTTCCACTAGCAGCAACATATATTTGTTTCAACGGCTG	1721
Db	2016	CTATAACAACATGAAATTTTCATCTAAAGACCAAGTGTGTGAGTGTCCAAATGAAG	2075
Qy	1722	GGTGTGCGGAGCTCCCTTTTACACCGTGTGATATTTACGGGAAGCGTGTGCTGAGTGT	1781
Db	2076	GGGTTTCCCAAGTATCTCTGACCGCTGCCACATCTATGGTACAGCTGTGCTGACTGCT	2135
Qy	1782	GGCTCGCGGAGACCTTACTGTGCTGGGATGGTGTCTGTCATGTTCTCGCTATTTTCCCA	1841
Db	2136	GGCTGCGCGGAGACCTTATTGCGCTGGGATGGCAATCTCTGTTCCAGATTTCTACCCA	2195
Qy	1842	CTGCAAGAGAGCAGCAAGACAGATATAAGAAATGGAGACCCACTGACTCATCTGTT	1901
Db	2196	CTGGGAAACCGAGGAGCGGAAGACAGATGTGAGACATGGAAACCCCACTGACTCAATG	2255
Qy	1902	CAGACTTACACCATGATTAATCACCATGGCCACAGCCCTGGAAGAGAGAATCATCTATGG	1961
Db	2256	GAGGATTTTAAAGGATTAAGAAATGACAGAAATGACAGCTGAAATTTGTCAGTATGGAG	2309

QY 1962 TAGAGAAATAGTACCAATTTTGGATGCAAGTCGAGAGAGCGCTGTATT 2021
Db |||||
Db 2310 TAAATAATACCACTTTTCTGGAGTGTGCCCAAGTCTCGCAGGCATCTATCAAGT 2369
QY 2022 GCAATTCAGAGGCGAATAGAGCGGAAAGAGAGATGAGTGGATGATCATATCA 2081
Db |||||
Db 2370 GGCTGTATACAGA---AAGACAAAGACAGGAGGAAAGAGGTTAAGCTGAATGAACGAATAA 2426
QY 2082 TCAGGACAGATCAAGGCTTCTGTACGTAGTCTACAACAGAGGATTCAGGCAATTAAC 2141
Db |||||
Db 2427 TAGCCATTCACAGGACTCTGTATCCGCTCTGTTCAGGGTCTGACCAAGGACTTTATC 2486
QY 2142 TCTGCCATCGGTGGAACTATGAGTTCATACAAACTCTTCTTAAGGTAAACCTCGAAGTCA 2201
Db |||||
Db 2487 ACTGCATTCTACAGAAATAGTTTCAAGCAGACCATAGCCAAAGATCACTTCAAAGTTT 2546
QY 2202 TTGACACAGCAGATTGG 2219
Db |||||
Db 2547 TAGATTCAAGAAATGGTG 2564

RESULT 10
US-09-813-290-3
; Sequence 3, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodin
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-813-290-3

Query Match 17.5%; Score 474.8; DB 4; Length 2349;
Best Local Similarity 53.9%; Pred. No. 3.9e-138;
Matches 1146; Conservative 1; Mismatches 948; Indels 33; Gaps 7;

QY 280 CAATGTGCCAAGCTGAAATATCTTACAAAGAAATGTTGGAATCCAAATGTGATCAC 339
Db 84 CAGTGTGCCCGCTCGGCTCTCTACCGAGACCTCTGTCTGCCAACCGCTCTGCCAT 143
QY 340 TTTCAATGGCTGGCCAAACAGCTCAGTGTATCATACCTTCTCTTTGGATGAGAAAGGAG 399
Db 144 CTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGA 203
QY 400 TAGGCTGTATGTTGGAGCAAGAGATACATATTTTCATTCGACCTGGTTAATATCAAG-- 457
Db 204 CGGCTCTTTCTGGTGGCTGGAGCGCTCTACTCTCTGCGGCTGGACAGGCAATGGCC 263
QY 458 -GATTTTCAAAGATGTTGTGCCAGATATCTTACACCAAGAGAGATGAATGCAAGTGGGC 516
Db 264 AGATCCCGGAGGTCCTGTGGCCACCGCAGCAGCAGAGAGGGAGGTGTTCGAA 323
QY 517 TGGAAAGACATCTCTGAAGAAATGTGCTAATTTTCAAGGTACTTAAGGCATATAATCA 576
Db |||||

Db 324 GGGAGAGATCCTTTGACAGAGTGCGCCAACTTCTGTGGGGTGTCTACAGCCTCACAACCG 383
QY 577 GACTCATTGTACGCTGTGGAACGGGGCTTTTTCATCCAATTTTCACCTACATTGAAT 636
Db |||||
Db 384 GACCACCTGTAGCTGTGGACCTTGGGGCTTTCAGCCACCTGTGCCCTCATCACAGT 443
QY 637 TGGACATCATCTGAGGAAATATTTTAAAGCTGGAGAACTCACATTTTGAAGAAACGGCG 696
Db |||||
Db 444 TGGCCACCG---TGGGAGCATGTCTCCACTGGAGCTGGCAGTGTGGAAGTGGCG 500
QY 697 TGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGAGAAT 756
Db |||||
Db 501 GGGGGCTGTCCCTCAAGAGCCCGCTCCCTTTTCCAGACCTTTCATAGACGGGAGCT 560
QY 757 ATACTCTGAACTGACAGCTGATTTTATGGGGGAGACTTTGTATCTTCCGAACCTTTGG 816
Db |||||
Db 561 GTACACGGGTCTCACTGTCTGCTTCTGGGGGAGAGGCCATGATCTTCCGAAGTGGAG 820
QY 817 GCACCACCAACCAATCAGGACAGAGCATGATTTCCAGGTGGCTCAATGATCCAAGTT 876
Db |||||
Db 621 TCCTGGCCAGCTCTGCGTTCGAC---TCTGACCAGAGTCTCTTGCACGACCCCGGT 677
QY 877 CATTAAGTCCCACTCATCTCAGAGAGTGACATCTCTGAAGATGACAAAGATATATTTT 936
Db |||||
Db 678 TGTGATGGCCCGCGGATCCCTGGAACCTCTGACCAAGCAATGACAAAGGTGTACTCTT 737
QY 937 CTTCCGTGAAAATG---CAATAGATGGAGAACACTCTCGAAAAGCTACTCAGCTAGAAT 993
Db |||||
Db 738 CTTCTGGAGAGCGTCCCTCGCCGATGGTGGCTCGAACCATGTCTCATGTGACGGCGT 797
QY 994 AGGTGAGATATGCAAGAAATGATTTTGGAGGACAGAAAGTCTGTGTAATAAATGACAAAC 1053
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Db 798 GGGCGCGCTGCTGCTGATGATGCTGGGGCCAGCGGTGCTGTGTGAACAAATGGAGCAC 857
QY 1054 ATTCTCAAAGTCTGTGATTTGCTAGTGCAGGTCCAAATGCAATGCACTGATCATTT 1113
Db |||||
Db 858 TTTCTCAAAGCCAGGCTGGTCTGCTCGTGGCCCGCTGTGTGGTGGCAGACCCACTT 917
QY 1114 TGATGAATCGAGGATGATTTCTTAATGAACCTTTTAAAGATCCTAAATTCAGTTGTATA 1173
Db |||||
Db 918 TGACAGCTAGAGATGTTCTCTGTGGCCCAAGCCGGAAGAGCCTCGAGGTGA 977
QY 1174 TGGAGTGTATACGACTTCCAGTAACATTTTCAAGGATCAGCCGCTGTGTATGATAGAT 1233
Db |||||
Db 978 CGCGCTGTTACAGACCGTCACTGCGCTGTTCAGGGCTTCGCGCTGTGTGTACCAT 1037
QY 1234 GAGTGTGAGAGGGTGTCTTGTGTCATATGCCCCACAGGATGACCCCACTATCA 1293
Db |||||
Db 1038 GGCAGACATCTGGGAGGTTTCAAACGGGCCCTTTTCCACCGAGATGGGCCCTCAGCACCA 1097
QY 1294 ATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGCCAGGACTTGTCCAGCAAAA- 1352
Db |||||
Db 1098 GTGGGGCCCTATGGGGCAAGGTGCCCTTCTCGCCCTGGCGTGTGCCCCAGCAAGAT 1157
QY 1353 -----CATTTGGTGGTTTGACTTACAAAGAACCTTCTGTATGATGTTTATAAC 1401
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Db 1158 GACCACAGCCAGGACGGCTTTTGGCAGCACCAAGGACTACCCAGATGAGTGTCTGCA 1217
QY 1402 CTTTGAAGAAGTCAATCCAGCCTGTAATCCAGTGTTCCTATGAACATCGCCCAAT 1461
Db |||||
Db 1218 GTTTCGCCAGGCCACCCCTCATGTTCTGCGCTGTGGGCCCTGCAATGGCCGCTGT 1277
QY 1462 AGTGAATCAAAACGGATGTAATTAATCAATTTTACAAATTTGCTGAGACCGAGTGGATGC 1521
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Db 1278 CTTTGTCAAGACCCACTTGGCCCGCAGCAGTACACAGATCGTGTGGACCGGTGGAGC 1337
QY 1522 AGAAGATGGAAGATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTGTCTTAAAGT 1581
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Db 1338 AGAGATGGGACCTACGATGTCTTTCTGGGAGTGTGACTCAGGCTCTGTGCTCAAGT 1397
QY 1582 AGTTTCAATTTCTTAAGGAGCTTGGTATGATTTAGAAGAGTTCGTCTGGAGAAATGAC 1641
Db |||||
Db 1398 CATGCTCTCCAGGACGGGGCTCAGCTGAACCTGAGGAAGTGGTCTTGGAGGAGCTCCA 1457

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QY 1642 AGTTTTCCGGAAACCGACTGCTATTTCAGCAATGAGAGCTTTCCACTAAGCAGCAACAAT 1701
Db |||||
QY 1458 GGTGTTTAAGGTGCCAACACCTATCACCAAAATGGAGATCTCTGTCAAAGGCAAAATGCT 1517
Db |||||
QY 1702 ATATATTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACGGTGTGATTTACGG 1761
Db |||||
QY 1518 ATACGTGGGCTCTCGGCTGGGTGGCCAGCTGGCGCTGCACCAATGTGAGACTTACGG 1577
QY 1762 GAAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTTGGGATGGTTCTGC 1821
Db |||||
QY 1578 CACTGCTGTGAGAGTGTGCTGGCCGGGACCATACTGTGCTGGATGGTGCCTC 1637
QY 1822 ATGTTCTCCTATTATTTCCCA---CTGCAAGAGAGCGCAACAGCAGCAAGATATAGAAA 1878
Db |||||
QY 1638 CTGTACCCACTACCGCCCGAGCTTTGGCAAGCGCGGTTCGCCCGCAGGACATCCGGCA 1697
QY 1879 TGGAGACCCACTGACTCACTGTTGAGACTTACACCATGATATACCATGGCCACAGCCC 1938
Db |||||
QY 1698 CGGCAACCTGCGCTGCACTGCTGGCCGAGCCAGGAGGAGGAGGAGTGGGACTTGT 1757
QY 1939 TGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCAATTTTGGAAATGCAAGTCCGAA 1998
Db |||||
QY 1758 GGCAGCCACCATGTTCTAGCGACCGGACACATAGCACCTTCTGGAGTGTGCTGCCAA 1817
QY 1999 GTGCGAGAGAGCGCTGCTATTGTCATTTCCAGAGCGGAAATGAGAGCGGAAAGAGA 2058
Db |||||
QY 1818 GTCTCCCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1877
QY 2059 GATCAGAGTGGATGATCATATATCAGGACAGATCAAGGCTTCTGCTAGCTAGTGTACA 2118
Db |||||
QY 1878 GGTGAAGACGACGAGCGAGTCTTGACACGAGCGGGGCTGCTGCTGCTGCTGCTGCTGCT 1937
QY 2119 ACAGAGAGATTCAGGCAATTAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2178
Db |||||
QY 1938 CGTTCGATGCGGACCTACCTGACCACTCTGGAGCAATGGCTTCTCCAGACTGT 1997
QY 2179 TCTTAAGGTAACCTCGAAGTCAATGACACAGAGCAATTTGGAAGAACTTCTTATATAAGA 2238
Db |||||
QY 1998 GGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2057
QY 2239 TGATGATGAGATGGCTTAAGACCAAGAAATGTCCAATAGATGACACCTAGGACAGAA 2298
Db |||||
QY 2058 GCCAAGACGACGAGGAGCCCGGAGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2111
QY 2299 GGTCTGTTACAGAGCTTCATCAGCTCATCAACACCCCAATCTCAACACGATGATGA 2358
Db |||||
QY 2112 GGCCTGGTCAAGGACATCTGAGCTCAATGGCTTGGCCAACTGCTGCTGCTGCTGCTGCTGCT 2171
QY 2359 GTTCTGTGAACAAGTTTGGAAAGGAC 2386
Db |||||
QY 2172 GTACTGTGAGCGGTGTGTCAGGGGC 2199

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```

RESULT 11
US-09-813-290-1
; Sequence 1, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; FILE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188

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; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-813-290-1

Query Match      17.5%; Score 474.8; DB 4; Length 2628;
Best Local Similarity 53.9%; Pred. No. 4,3e-138;
Matches 1146; Conservative 1; Mismatches 948; Indels 33; Gaps 7;

QY 280 CAATGTGCCAAGCGCTGAAATTTATCTCAAAAGAAATGTTGGAAATCCAAACAATGTGATCAC 339
Db |||||
QY 340 TTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTGGATGAGAAACGAG 399
Db |||||
QY 423 CTTTCTGGGCCCGCCAGGGCTCCTGAACTCCAGGCCATGTACCTAGATGAGTACCGAGA 482
QY 400 TAGGCTGTATGTTGGAGCAAGGATCAATATTTTCATTCGACCTGTTTAATATCAAG-- 457
Db |||||
QY 483 CCGCCTCTTTCTGGGTGGCTGGACCGCCTCTACTCTCTGCGGCTGGACCGGCAATGGCC 542
QY 458 -GATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAATGCAAGTGGGC 516
Db |||||
QY 517 TGGAAAAGACATCTCTGAAAGAAATGCTAAATTTTCATCAAGGTACTTAAGGCAATATAATCA 576
Db |||||
QY 603 GGGAGAGATCTCTTTGACAGAGTGGCCAACTTCTGCGGGTGTCTACAGCCTCACAAACG 662
QY 577 GACTCACTTGTAGCTGTGGAAACGGGGCTTTTTCATCCAATTTGCACCTACATTTGAAT 636
Db |||||
QY 663 GACCCACCTGTAGCTGTGGCACTGGGGCTTCCAGCCCTCTGCGCCTCATCACAGT 722
QY 637 TGGACATCATCTCTGAGGCAATATTTTAAAGCTGAGAACTCACATTTTGAAGAACGGCG 696
Db |||||
QY 723 TGGCCACCG---TGGGGAGCATGTGCTCCACTGGAGCCTGGCAGTGTGAAAGTGGCG 779
QY 697 TGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAAAT 756
Db |||||
QY 780 GGGCGGTGCTCTACAGAGCCCGAGCTCCCTTTGCCAGCACTTCATAGACGGGAGCT 839
QY 757 ATACTCTGGAACCTGAGCTGATTTTATGGGGGAGACTTTGCTATCTTCCGAACTCTTGG 816
Db |||||
QY 840 GTACACGGGTCTCACTGTCTGACTTCTGCGGCGAGAGGCCATGATCTTCCGAAGTGGAG 899
QY 817 GCACCAACCAATCAAGACAGAGCATGATTTCCAGGTGGCTCAATGATGATCAAGT 876
Db |||||
QY 900 TCTTGGCGAGCTCTGCGTTCCGAC---TCTGACAGAGTCTCTTGCACGACCCCGGT 956
QY 877 CATTAAGTCCCACTCATCTCAGAGAGTGAACAATCTCTGAAGATGACAAAGTATCTTTT 936
Db |||||
QY 957 TGTGATGGCGCCCGATCCCTGAGAACTCTGACCCAGGACATGACAAAGTGTACTTCT 1016
QY 937 CTTCCGTGAAATG---CAATAGATGGAGAACACTCTGGAAGAACTCTACGCTTGAAT 993
Db |||||
QY 1017 CTTCTCGGAGACGGTCCCTCGCCCGATGTTGGTGGCTCGAACCATGTCTCTGACGCGCT 1076
QY 994 AGGTGAGATATGCAAGAAATGACTTTGGAGGGGACAGAGTCTGTTGAATTAATGGAAC 1053
Db |||||
QY 1077 GGGCGCGCTGCTGCGTGAATGATGCTGGGGGCCAGCGGCTGCTGGTGAACAAATGGAGCA 1136
QY 1054 ATTTCTCAAGAGTCTGCTGATTTGCTCAGTGGCAGGTCCAAATGGCAATGACACTCAT 1113
Db |||||
QY 1137 TTTCTCAAGGCGAGGCTGGTCTGCTGCTGCGCGGCTCTGTTGGCGGAGGCCACTT 1196
QY 1114 TGATGAACCTGCAAGATGATTTCTTAATGAACCTTTTAAAGATCTTAAAGATTCAGTGTGATA 1173

```

Db 1197 TCACAGCTAGAGATGTGTTCTCTGTGTGGCCCAAGGCCGGAGAGCGCTCGAGGTGTA 1256
Qy 1174 TGGAGTGTTCAGACTTCACGTAACATTTCAAGGGATCAGCCGTGTGTATAGCAT 1233
Db 1257 CGCGTGTTCAGACCGTCAGTGCCTGTTCAGGGCTTCGCGCTGTGTGTACCAT 1316
Qy 1234 GAGTGATGTGAAGGGTGTTCCTTGTGTCCATATGCCACAGGGATGGAACCAATATCA 1293
Db 1317 GCGACATCTGGAGGTTTCAACGGGCCCTTTCGCCACCGAGATGGCCTCAGCACA 1376
Qy 1294 ATGGTGCTTATCAAGAGAGTCCCTATATCCACGGCCAGAACTTGTCCAGCAAAA- 1352
Db 1377 GTGGGGGCCATATGGGGCAAGTGCCTTCCCTCGCGCTGTGGCGTGTGCCCGCAGAGAT 1436
Qy 1353 -----CATTTGTGTGTTTGAATCTACAAAGGACCTTCTCTGATGATGTTATAAC 1401
Db 1437 GACCCACAGCCAGGACGGCTTTTGGCAGCAACCAAGGACTACCCAGATGAGTCTGCA 1496
Qy 1402 CTTTTCAGAGAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCAAT 1461
Db 1497 GTTTCGCCGAGCCACCCCTCATGTCTGGCTGTGGCTTCGACATGGCCGCTGT 1556
Qy 1462 AGTGATCAAAACGGATGAATATTAATTAACAATAATGTGTAGACCGAGTGGATGC 1521
Db 1557 CCTTGTCAAGACCCACTGGCCAGCAGCTACACAGATCGTGTGTGACCGCGTGGAGGC 1616
Qy 1522 AGAAGTGCACAGTATGATGTATGTTATCGAAGACAGATGTGGGACGTTCTTAAAGT 1581
Db 1617 AGAGATGGACCTACGATGTCAATTTCTTGGGACTGACTCAGGGTCTGTGCTCAAAAGT 1676
Qy 1582 AGTTTCAATTCCTAAGGAGACTTGTATGATTTAGAAGAGTTCCTGCTGGAGAAATGAC 1641
Db 1677 CATCGCTCCAGGACGAGGGCTCAGCTGAACCTGAGGAGTGTCTGGAGAGCTCCA 1736
Qy 1642 AGTTTTTCGGGAACGACTGTATTTTCAAGATGAGCTTTCCACTAAGCAGCAACAAT 1701
Db 1737 GGTGTTTAAGGTGCCAACACCTATCACCGAATGAGATCTCTGTCAAAAGGCAAAATGCT 1796
Qy 1702 ATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATTTACGG 1761
Db 1797 ATACGTGGGCTCTCGGCTGGGTGTGGCCAGCTGGCTGCGCTGCACCAATGTGAGACTTACGG 1856
Qy 1762 GAAAGCGTGTGTGAGTGTGCTCGCCGAGACCTTTACTGTCTTGGAGTGTCTTGC 1821
Db 1857 CACTGCTGTGCAGAGTGTGCTGCGCGGGACCCATCTGTGCTGGAGTGTGCTC 1916
Qy 1822 ATGTTCTCGTATTTTCCCA----CTGCAAGAGACGCAACAGCAGCAAGATTAAGAAA 1878
Db 1917 CTGTACCCACTACCGCCCGAGCTTTGGCAAGCGCGGTTCCGCGCGCAGGACATCCGGCA 1976
Qy 1879 TGGAGACCCACTGACTCACTGTTCAAGACTTACACCATGATATACCATGGCCACAGCCC 1938
Db 1977 CGGCAACCTGCGCTGCTGCTGGCCAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAG 2036
Qy 1939 TGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTACACATTTTGGATGCAATCCGAA 1998
Db 2037 GSCAGCCCATGGTCTACGGCACGAGCAGCAATAGCACTTCTTGGAGTGTCTGCCCAA 2096
Qy 1999 GTCCAGAGAGCGCTGTCTATTTGGCAATTCAGAGGGCAATGAAGAGCGGAAAGAGAGA 2058
Db 2097 GTCTCCCGAGCTGTGTGCGCTGTCTTGTGAGAGGCGCAGGGGATGAGGGGCTGACCA 2156
Qy 2059 GATCAGAGTGAATGATATATATCATCAGGACAGATCAAGGCTTCTGCTACGTPAGTCTACA 2118
Db 2157 GGTGAAGACGACGAGGAGTCTTGCAACGAGCGGGGCTGTCTTCCGAGCGCTTAG 2216
Qy 2119 ACAGAGAGATTCAGGCAATTAACCTCTGCCATCGGTGGAAACATGGGTTTCAACAACTCT 2178
Db 2217 CGGTTTCGATGGGGCACCTACACCTGCACCACTCTGGAGCATGCTCTCTCCAGACTGT 2276
Qy 2179 TCTTAAGGTAACTTGGAGTCAATTTGACACAGAGCATTTGGAGAACTTCTTTCATAAAGA 2238
Db 2277 GGTCCGCTGTGCTGTGGTGTGATTTGTGGCTTCAAGCTGGGCAACCTGTTCCCTCCGGA 2336

Qy 2239 TGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAA 2298
Db 2337 GCCAAAGCAGAGAGCCCGCAGCCCGGGAGGCTGGCTTCCACCCACC-----CAA 2390
Qy 2299 GGTCTGGTACAGAGACTTCATGCACTCATCAACCAACCCCAATCTCAACAGATGATGA 2358
Db 2391 GGCCTGGTACAGAGACATCTCTGAGCTCATTTGGCTTCCCAACCTGCCCCGGGTGATGA 2450
Qy 2359 GTTCTGTCAACAAGTTTGGAAAAGGGAC 2386
Db 2451 GTACTGTAGCGCGTGTGTGTCAGGGC 2478

RESULT 12

US-09-813-290-5
; Sequence 5, Application US/09813290
; Patent No. 6815538
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; TITLE OF INVENTION: No. 6815538el Human Secreted Proteins and Polynucleotides Encodir
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3568
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-813-290-5

Query Match 17.5%; Score 473.6; DB 4; Length 3568;
Best Local Similarity 53.9%; Pred. No. 1.3e-137;
Matches 1146; Conservative 0; Mismatches 949; Indels 33; Gaps 7;

Qy 280 CAATGTGCCAAGGCTGAAATTTATCTACAAAGAAATGTTGGAATCCAAATGTGATCAC 339
Db 917 CAGTGTGCCCCGCTGCGGCTCTCTACCGAGACCTCTCTGTGCAACCGCTCTGCCAT 976
Qy 340 TTTCATGGCTTGGCCAAACAGCTCCAGTATCATACCTCTTTTGGATGAGAACGAG 399
Db 977 CTTTCTGGGCCCCCAGGGCTCTCTGAACCTCCAGGCCATGTACCTAGATGATACCGAGA 1036
Qy 400 TAGGCTGTATGTGGAGCAAGAGATCATATTTTTCATTCGACCTGTGTTAATATCAAG-- 457
Db 1037 CGGCTCTTTCTGGTGGCTTGGAGCCCTCTACTCTCTGGCGTGGACCGCATGCC 1096
Qy 458 -GATTTTCAAGAGTGTGTGCCAGTATCTTACACAGAGAGATGAATGCAATGCAATG 516
Db 1097 AGATCCCGGAGGTCTGTGCCACCGCAGCAGGAGGAGGAGTGTGTTTCGAAA 1156
Qy 517 TGGAAAACACATCTGGAAGATGTCTAATTTTCATCAAGTACTTAAGGCTAATAACA 576
Db 1157 GGAAGAGATCCTTTGACAGAGTGGCCAACTTCTGTGGGTGCTTACAGCTTCAACCG 1216
Qy 577 GACTCAGTGTACGCTGTGGAACCGGGGCTTTTTCATCCAAATTTGCACCTACATTGAAT 636
Db 1217 GACCCACCTGTAGCTGTGCACTGGGGCTTCCAGGCCCTGTGCCCTCATCAGCT 1276
Qy 637 TGGACATCATCTGTAGGAGCAATATTTTAAAGCTGGAGAACTCACATTTTGAACACGGCGC 696

[illegible]

Db	2351	ATACGTGGGCTCTCGCGTGGGTGGTGGCCAGCTGCGGCTGCACCAATGTGAGACTTACGG	2411
Qy	1762	GAAGCGTGTCTGCTAGTGTTCCTTCGCCCGAGACCCCTTACTGTGCTTGGGATGGTTCTGC	1821
Db	2411	CACCTGCTGTGCAGAGTGTCTGCTTGGCCCGGAGCCCACTACTGTGCTGGGATGGTGCCTC	2470
Qy	1822	ATGTTCTCGCTATTTTCCCA--CTGCAAGAGACGCACAAGACGACAAGATATAGAAA	1878
Db	2471	CTGTACCACCACTACCGGCCCAAGCCTTGGCAGCGCCGGTTCCGCGGAGACACATCCGGCA	2530
Qy	1879	TGGAGACCCCACTGCACTCACTGTTTCAGACTTACACCATGATAATCACCATGGCCACAGCCC	1938
Db	2531	CGGCAACCCCTGCGCTGCAGTGCCTGGCCAGAGCCAGGAAGAAGAGCAGTGGGACTTGT	2590
Qy	1939	TGAAGACAGAAATCATCTATGGTGTAGAGAAATAGTAGACATATTTTGGAAATGCAGTCCGAA	1998
Db	2591	GGCAGCCACCATGGTCTTACGGCACGGAGCAATAGCACCTTCTCTGGAGTGCCTTGCCCA	2650
Qy	1999	GTCCGACAGAGCGCTGTGTTATTGGCAATTCACAGAGCGAAATTCAGAGCGCAAAAGAAGA	2058
Db	2651	GTCTCCCCAGGCTGCTGTGGCTGGCTCTTTGCAGAGGCCAGGGGATGAGGGGCTTGACCA	2710
Qy	2059	GATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCGTCTTGCTACGTTAGTCTTACA	2118
Db	2711	GGTGAAGACGCAACGAGCGAGTCTTTGCACACGGAGCGGGGCTGCTGTTCCGCGAGGCTTAG	2770
Qy	2119	ACAGAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTCATACAAACTCT	2178
Db	2771	CCGTTTCGATCGGGGACCTTACACCTGCACCACTCTGGAGCATGGCTTCTCCCGAGACTGT	2830
Qy	2179	TCTTAAAGTAAACCTCGGAAGTCAATTGACACAGAGCATTTGGAAGAACTTCTTCATAAAGA	2238
Db	2831	GGTCGGCCTGGCTCTGTGTGGTGTATTGTGGCTCACAGCTGGACAACTGTTCCCTCCGGA	2890
Qy	2239	TGATGATGAGATGGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACCTTAGCCAGAA	2298
Db	2891	GCCAAAGCCAGAGAGCGCCCGAGCCCGGGGAGGCGCTGGCTTCCACCCACC-----CAA	2944
Qy	2299	GGTCTGTTACAGAGACTTCATGCACTCATCAACACGCCCAATCTCAACACGATGGATGA	2358
Db	2945	GGCCTGGTACAGAGACATCTGCACTCATTTGGCTTGCACCACTGGCCCGGGTGGATGA	3004
Qy	2359	GTTCCTGAAACAAGTTTGGAAAAAGGGAC	2386
Db	3005	GTACTGTGACGCGTGTGGTGCAGGGC	3032

RESULT 13

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RESULT 13
US-09-513-999C-2555
; Sequence 2555, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2555
; LENGTH: 229
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..229
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: 110
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 113
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 116
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 122
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 28
; OTHER INFORMATION: Xaa=Glu or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 29
; OTHER INFORMATION: Xaa=Ala or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 30
; OTHER INFORMATION: Xaa= * or Lys
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 32
; OTHER INFORMATION: Xaa=Gly or Ser
; OTHER INFORMATION: Xaa=Gly or Ser
US-09-513-999C-2555

Query Match 5.1%; Score 138.8; DB 4; Length 229;
Best Local Similarity 97.0%; Pred. No. 4.6e-33; Mismatches 0; Indels 2; Gaps 2;
Matches 159; Conservative 3;

QY 118 TTCCAGATTGTTGAACCTCTCTGCGCCACAAATACAGGAAGAACT-AAAAGCAGCA 176
DB 66 TTTCAGATTGTTGAACCTCTCTGCGCCACAAATACAGGAAGAACT-AAAAGCAGCA 125
QY 177 AAGGACCTACAGCGTCTCAGCATGGCTGTTAACTAGGATTGTTCTTTCTGGG 236
DB 126 AAGGACCTACAGCGTCTCAGCATGGCTGTTAACTAGGATTGTTCTTTCT-GG 184
QY 237 GAGTATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGAC 280
DB 185 GAGTATTACTTACAGCAAGCAAACTATCAGAAATGGGAAGAC 228

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RESULT 14
US-09-520-781-29
; Sequence 29, Application US/09520781
; Patent No. 6689866
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
; FILE REFERENCE: 15966-540 No. 6689866el Polynucleotides
; CURRENT APPLICATION NUMBER: US/09/520,781
; CURRENT FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: USSN 60/123,667
; PRIOR FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1890)
US-09-520-781-29

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Query Match 4.6%; Score 125; DB 4; Length 1890;

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Best Local Similarity 50.5%; Pred. No. 4.3e-28;
Matches 488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;

QY 689 AACGCCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATAGAT 748
DB 430 AGCGGAATGGCCAGATGCCCATATGATGCCAAACATGCCAAGCTGTTCAGAT 489
QY 749 GGAGAAATATATCTCTGGAACTGACGTCTATTTATGGGGCGAGACTTTGCTATCTTCCGA 808
DB 490 GGAAAACTATATCTCTAGCCACAGTGACTCTCTTGGCAATGACGAGTCAATTTACCGG 549
QY 809 ACTCTTGGGCACACACCACCAATCAGGACAGACATGATTCAGGTGGCTCAATGAT 868
DB 550 AGTCTTGGAGAAAGCCCTACCTCGGACCGTCAAGCAGGATTCAAAATGGTTGAAGAA 609
QY 869 CCAAGTTTCATTAGTGCCCACTCATCTCAGAGAGTGACATCTCTGAAGATGACAAAGTA 928
DB 610 CCATACCTTTTGTTCAGCCGTGGA-----TTACGGAGATTATATC 648
QY 929 TACTTTTCTTCCGTGAAAATGCAATAGATGGAGAACACTCTGGAAAAGCTACTCACGCT 988
DB 649 TACTTCTTTCAGGGAATAGCAGTGAGTATACACATGGGAAAGTAGTTTTCCTCA 708
QY 989 AGAATAGTCTAGATATGCAAGAATGACTTTTGGAGG---GCAACAGAGTCTGGTGAATAAA 1045
DB 709 AGAGTGGCTCAGGTTTGTAGAAATGATATGGAGGATCTCAAAGAGTCTCTGGAGAAACAG 768
QY 1046 TGGACAAATTCCTCAAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGCATGAC 1105
DB 769 TGGACGTCTCTCTGAAGCGCGTTGAACCTGCTCAGTCTCTGG-----AGACTCTCAT 822
QY 1106 ACTCATTTTGTGATGAATCAGAGATGATTTCTTAATGAACCTTTAAAGATCTCTAAATCCA 1165
DB 823 TTTTATTTCAACATTTCTCAGGAGGTACAGATGATGATTCATCAACGGGGTGAT--- 879
QY 1166 GTTGATATAGGAGTGTTCAGACTTCCAGTAAACATTTTCAAGGGATCAGCGGTGTGTATG 1225
DB 880 GTTGCTCTGGCAACGTTTCTTACACCTTATAACAGCATCCCTGGGTCTCAGTCTGTGCC 939
QY 1226 TATAGCATGAGTGTGAGAGAGGTGTTCTTGTCTCATATGCCACAGGATGACCC 1285
DB 940 TATGACATGCTTGACATTTGCCAGTGTTTTACTGGGAGATTCAAGGAACAGAAAGTCTCT 999
QY 1286 AACTATCAATGGGTGCC---TTATCAAGGAAGAGTCCCTATCCACGGCCAGGAACTTGT 1342
DB 1000 GATTCACCTGGACACACAGTTCCTCTCATGAACGAGTTCTTAAGCCACAGCCAGGTGTGT 1059
QY 1343 CCCAGCAAA---ACATTTGGTGGTTTGACTCTCAAAAGGACCTTCTCTGATGATGTTATA 1399
DB 1060 GCTGGCTCATCTCCTTAGAAAGATATGCAACCTCCAATGAGTTCCTCTGATGATACCTGT 1119
QY 1400 ACCTTTGCAGAGTATCCAGCCATGACATCCAGTGTTCCTTATGAACATCGCCCA 1459
DB 1120 AACTTTCATCAAGACGACCCCTCATGATGAGGAGTGCCTTCATCTTCAACAGGGCA 1179
QY 1460 ATAGTGAATCAAAACGGATGTAATTTATCAATTTTACAAATTTGCTAGACCGAGTGGAT 1519
DB 1180 TGGTCTCTGAGAACATGTCAGATACCGCTTACCAAAATTTGCTAGTGAACACAGTGTCT 1239
QY 1520 GCAGAAATGACAGATGATGATGTTATGTTATCGGAAACAGATGTTGGACCGTCTTTAAA 1579
DB 1240 GGGCCATATCAGAAATCAGACTGTGGTTTCTCTGGGATCAGAGAGGGAATCATCTTTGAAG 1299
QY 1580 GTAGTTTCAATCTCAGGAGACTTGGTATGATTTAGAGAGGTTCTCTCGAAGAAATG 1639
DB 1300 TTTTGGCCAGAAATAGGAAATAGTGGTTTCTTAAATGACAGCTTTTCTCTGGAGGATG 1359
QY 1640 ACAGTTT 1646
DB 1360 AGTGTTT 1366

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RESULT 15

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US-09-976-594-1002
; Sequence 1002, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 1002
; LENGTH: 2278
; TYPE: DNA
; ORGANISM: Homo sapiens.
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673
US-09-976-594-1002

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Query Match	4.6%; Score 125; DB 4; Length 2278;
Best Local Similarity	50.5%; Pred. No. 4.9e-28;
Matches	488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;
Qy	689 AACGGCGTGGGAAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAATAGAT 748
Db	
Qy	758 AGCGGAATGCCAGATGCCCATATGATGCCAAACATGCCAACGTTGCACCTGTTTGCAGAT 817
Db	
Qy	749 GGAGAAATTACTCTCGAACTGCGAGCTGATTTTATGGGGGAGACTTTGCTATCTTCCGA 808
Db	
Qy	818 GGAATACTACTCAGCCACAGTGACTTCTCTGCCATTGACGAGTCATTTACCGG 877
Db	
Qy	809 ACTCTGGGCACCAACCCCAATCAGACAGACGAGCATGATTCAGGTGGCTCAATGAT 868
Db	
Qy	878 AGTCTTGGAGAAAGCCCTACCTCGCGACCGTCAAGCAGCATTCAAAATGGTTGAAAGAA 937
Db	
Qy	869 CMAAGTTTCATTAGTGGCCACTCATCTCAGAGAGTGACAAATCCTGGAAGATGACAAAGTA 928
Db	
Qy	938 CCTACTTTTGTTCGAAGCGGTGGA-----TTACGGAGATTATATC 976
Db	
Qy	929 TACTTTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAGACTACTCAGCCT 988
Db	
Qy	977 TACTTCTCTTCAGGSAATAGCAGTGGAGTATAACACCATGGGAAAGGTAGTTTCCCA 1036
Db	
Qy	989 AGAATAGTTCAGATATGCAAGATGACTTTTGGAGG---GCACAGAACTCTGGTGAATAAA 1045
Db	
Qy	1037 AGAGTGCTCAGGTTGTAGATGATATGGAGGATCTCAAGAGTCTTGGAGAAACAG 1096
Db	
Qy	1046 TGGACAACTTCTCAAAGCTCGTCTGATTTGCTCAGTGGCAGGTCCAAATGGCATTTGAC 1105
Db	
Qy	1097 TGGACGTCGTTCTGAAGCGCGCTGCACTGCTCAGTTCCTGG-----AGACTCTCAT 1150
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Qy	1166 GTTGTATATGGAGTGTTTACGACTTCAGTAAACATTTTCAAGGATCAGCGGTGTGTATG 1225
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Qy	1208 GTTGCTCTGGCAACGTTTCTACACCTTATAACAGCATCCCTGGGTCTGCAGTCTGTGCC 1267
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Qy	1226 TATAGCATGATGATGTGAGAAGGGTGTCTCTCGTCCATATGCCACAGGATGGACCC 1285
Db	
Qy	1268 TATGACATGCTTGACATGGCCAGTGTTTTACTGGAGATTCAGGAAACAGAGTCTCTCT 1327
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Db	
Qy	1343 CCCAGCAAA---ACATTTGGTGGTTTTTGACTCTTCAAAAGGACCTTCTGTATGATGTATATA 1399
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Qy	1400	ACCTTTCCAAAGAAAGTCATCCAGCGCATGTACAATCCAGATGTTTCCTATGAAACAATCGCCCCA	1459
Db	1448	AACTTCATCAAGACGCAACCGGCTCATGGATGAGCGAGTCGCCCTCATCTTCCAACAGGCCA	1507
Qy	1460	ATAGTGATCAAAACGGATGTAAATATCAATATTCACAAATGTCGTAGACCGAGTGGAT	1519
Db	1508	TGGTTCTCTGAGAACATGGTCAGATACCGGCTTACCNAANATTCAGATGGACACAGTGCT	1567
Qy	1520	GCAGAAGATGGACAGTATGATGTTATCGGAACAGATGTTGGACCGTTCCTTAAA	1579
Db	1568	GGGCCATATCAGAATCACTGTGTGTTTTTCTGGGATCAGAAAGGGAATCATCTTTGAAG	1627
Qy	1580	GTAGTTTTCAATTCCTAAGGAGACTTGATATGATTATGAACAGAGTTCTGCTGGGAAGAAATG	1639
Db	1628	TTTTTGGCCAGATAGGAAATAGTGGTTTTCTAAATGACACGCTTTTCTCTGGAGGAGATG	1687
Qy	1640	ACAGTTT	1646
Db	1688	AGTGTTT	1694

Search completed: March 10, 2005, 09:43:44
Job time : 501 secs

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 Db 181 GACCTACAGCCTGTCAGCATGGCTGGTTAACTAGGATGCTGCTTTCTGGGAGT 240
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 Db 301 ATCTTACAAAGAAATGTTGGAAATCCAAATGTGATCACTTTCAATGGCTGGCCAAACAG 360
 Qy 361 CTCCAGTTATCATACCTCTCTTTGAGTGAAGAACGAGTGGCTGATGTTGGAGCAAA 420
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 Qy 661 TTTTAACTGGAGAACTCACATTTTGAAGAACGCGCTGGGAAGAGTCCATATGACCTAA 720
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 Db 781 TATGGGCGAGATTTGCTATCTTCCGAACCTTGGGCAACCAACCCAAATCAGGACAGA 840
 Qy 841 GCAGATGATCCAGGTGGCTCAATGATCCAAAGTTCATTTAGTGCCCACTCATCTCAGA 900
 Db 841 GCAGATGATCCAGGTGGCTCAATGATCCAAAGTTCATTTAGTGCCCACTCATCTCAGA 900
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 Qy 1021 AGGGCAGAGATCTGGTGAATTAATGACAACTTCTTCAAGCTCGCTGATTTGCTC 1080
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 Db 1261 TCCATATGCCACAGGGATGGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCC 1320
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 Db 1741 ACACGGTGTGATATTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTA 1800
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 Qy 1921 TCACCATGGCCACAGCCTGGAAGAGAAATCATCTATGCTGTAGAGATAGTACACATT 1980
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 Db 2161 TGGGTTCATACAAACTCTTTTAAAGTAAACCTTGAAGTCAATTCAGACAGAGCATTTGGA 2220
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Db |||||
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Qy |||||
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Db |||||
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Qy |||||
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Qy |||||
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Db |||||
2169 GATCAGTTCTGTGAACAAAGTTTGAAGAGGACCGAAGAAACAACTGCGCAAGGCCAGG 2228
Qy |||||
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RESULT 3
US-10-097-340-283
; Sequence 283, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen ZHANG
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-283

Query Match 92.6%; Score 2508.4; DB 14; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 313 AATGTTGAATCCCAACAAATGATGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 372
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QY 373 TACCTTCCTTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
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QY 433 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTGTTGGCCAGTAGTCTTACAC 492
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QY 673 GAACTCACATTTTGAACCGGCGTGGGAAGAGTCATATGACCTCAATGCTGCTGACAGC 732
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Db 849 TCTGGTGAATAAATGGACAAACATTCCTCAAAGCTGCTGATTTGCTCAGTGCCAGGTCC 908
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QY 1873 AAGAAATGGAGACCCACTGACTCACTGTTTCCAGACTTTTACACCATGATAATCACCATGGCCA 1932
Db 1689 AAGAAATGGAGACCCACTGACTCACTGTTTCCAGACTTTTACACCATGATAATCACCATGGCCA 1748
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Db 1749 CAGCCTTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGACAATTTTGGAAATGCGAG 1808
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QY 2113 TCTCAACAGAAAGATTCAGGCAATTCCTCTGCCATGCGGTGGAAACATGGGTTTCATACA 2172
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QY 2173 AACTCTTCTTAAGGTAAACCTTGGAAAGTCATTGACACAGAGCAATTTGGAAAGAACTTCTTCA 2232
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QY 2413 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCCAAGATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTTAGA 2532
Db 2289 CAGGAGGACCCCAAGATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTTAGA 2348
QY 2533 AACCTCAACAAAGTAGAAACCTTGGCTAGACAAATTAAGTGAAGAAACAAATTAACAT 2592

Db 2349 AACCTCAAAAGTAGAAGCTTGCCTAGACAATACTGGAACAAACAAATCAATATACAT 2408
 Qy 2593 GAACCTTTTTCATGGCAATATGTTGGATGTTTACAAATGGTGGGAATTCAGCTGAGTTCCA 2652
 Db 2409 GAACCTTTTTCATGGCAATATGTTGGATGTTTACAAATGGTGGGAATTCAGCTGAGTTCCA 2468
 Qy 2653 CCAATTATAAATTAATCAATGAGTAACCTTCTCAATAGCTTTTTCCTCC 2702
 Db 2469 CCAATTATAAATTAATCAATGAGTAACCTTCTCAATAGCTTTTTCCTCC 2518

RESULT 4
 US-10-262-538-9
 ; Sequence 9, Application US/10262538
 ; Publication No. US20030113324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alitalo et al
 ; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
 ; FILE REFERENCE: 28967/37564
 ; CURRENT APPLICATION NUMBER: US/10/262,538
 ; CURRENT FILING DATE: 2002-09-30
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 2530
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (16)..(2331)
 US-10-262-538-9

Query Match 92.6%; Score 2508.4; DB 15; Length 2530;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 193 CTGAGCATGGGCTGGTTAACTAGGATGCTGTCTTTCTGGGAGGATTAATTTACAGC 252
 Db 9 CTGAGCATGGGCTGGTTAACTAGGATGCTGTCTTTCTGGGAGGATTAATTTACAGC 68
 Qy 253 AGAGCAAACTATCAGATGGGAAGAAACAATGTCGAAGGCTGAATTTATCCTACAAGA 312
 Db 69 AGAGCAAACTATCAGATGGGAAGAAACAATGTCGAAGGCTGAATTTATCCTACAAGA 128
 Qy 313 AATGTTGAATCAACAATGTGATCACTTTCAATGCTTGGCCCAACAGCTCCAGTTATCA 372
 Db 129 AATGTTGAATCAACAATGTGATCACTTTCAATGCTTGGCCCAACAGCTCCAGTTATCA 188
 Qy 373 TACCTTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT 432
 Db 189 TACCTTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATAT 248
 Qy 433 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCGAGTATCTTACAC 492
 Db 249 TTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATGTTGGCCGAGTATCTTACAC 308
 Qy 493 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTTTCAT 552
 Db 309 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTTTCAT 368
 Qy 553 CAAGGTACTTAAGGCATATAATCAGATCACTTGTACGCTGTGGAACGGGGGCTTTTCA 612
 Db 369 CAAGGTACTTAAGGCATATAATCAGATCACTTGTACGCTGTGGAACGGGGGCTTTTCA 428
 Qy 613 TCCAAATTCACCTACATTAATTTGAAGTGGACATCATCTGAGGACAATATTTTAAGCTGA 672
 Db 429 TCCAAATTCACCTACATTAATTTGAAGTGGACATCATCTGAGGACAATATTTTAAGCTGA 488
 Qy 673 GAACCTCACATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 732
 Db 489 GAACCTCACATTTTGAACCGGCGGTGGGAAGAGTCCATATGACCTCAAGCTGCTGACAGC 548
 Qy 733 ATCCCTTTTATAGATGGGAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGCGAGA 792

Db 549 ATCCCTTTTATAGATGAGATATATATCTTGGAACTCGAGCTGATTTTATGGGGGAGA 608
 Qy 793 CTTTGCTATCTTCCGAACTCTTGGGCAACAACCAATCAAGGACAGAGCAGATGATTC 852
 Db 609 CTTTGCTATCTTCCGAACTCTTGGGCAACAACCAATCAAGGACAGAGCAGATGATTC 668
 Qy 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGGCCCACTCATCTCAGAGAGTGACATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTGGCCCACTCATCTCAGAGAGTGACATCC 728
 Qy 913 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAACTCTCTGG 972
 Db 729 TGAAGATGACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGAGAACTCTCTGG 788
 Qy 973 AAAAGCTACTCAGCTAGATAGTGCAGATATGCAAGAAATGACTTTGGAGGGCACAAGA 1032
 Db 789 AAAAGCTACTCAGCTAGATAGTGCAGATATGCAAGAAATGACTTTGGAGGGCACAAGA 848
 Qy 1033 TCTGGTGAATAAATGGACAAATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 1092
 Db 849 TCTGGTGAATAAATGGACAAATTCCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC 908
 Qy 1093 AAATGGCATTGACACTCATTTTGTAGTGAATCGAGGATGTATTCCTAATCAATTTAAAGA 1152
 Db 909 AAATGGCATTGACACTCATTTTGTAGTGAATCGAGGATGTATTCCTAATCAATTTAAAGA 968
 Qy 1153 TCCTAAATAATCGAGTTGATATGAGAGTGTATCGACTTCCAGTAACTTCAAGGGATC 1212
 Db 969 TCCTAAATAATCGAGTTGATATGAGAGTGTATCGACTTCCAGTAACTTCAAGGGATC 1028
 Qy 1213 AGCCGTGTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
 Db 1029 AGCCGTGTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1088
 Qy 1273 CAGGATGAGACCCAACTATCAATGGTGCTTTATCAAGGAAGAGTCCCTATCCAGGCC 1332
 Db 1089 CAGGATGAGACCCAACTATCAATGGTGCTTTATCAAGGAAGAGTCCCTATCCAGGCC 1148
 Qy 1333 AGGAATTTGTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1392
 Db 1149 AGGAATTTGTCAGCAAAACAATTTGGTGGTGTGACTCTCAAGAGGACCTTCTGATGA 1208
 Qy 1393 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTAACATCAAGTGTCTTCTATGAAACA 1452
 Db 1209 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTAACATCAAGTGTCTTCTATGAAACA 1268
 Qy 1453 TCGCCCAATAGTATCAAAACGGATGTAATTAATCAATTTACAAATTTGCTAGACCG 1512
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 Qy 1513 AGTGGATGCAAGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1572
 Db 1329 AGTGGATGCAAGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1388
 Qy 1573 TCTTAAAGTGTCTTCAATTTCTAAGGACCTTGGTATGATGATGATGATGATGATGATGATGATGAT 1632
 Db 1389 TCTTAAAGTGTCTTCAATTTCTAAGGACCTTGGTATGATGATGATGATGATGATGATGATGATGAT 1448
 Qy 1633 AGAAATGACAGTTTTCGGGAAACCGATGCTATTTTACAGCAATGGAGCTTTCCACTAAGCA 1692
 Db 1449 AGAAATGACAGTTTTCGGGAAACCGATGCTATTTTACAGCAATGGAGCTTTCCACTAAGCA 1508
 Qy 1693 GCACACATATATTTGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGGA 1752
 Db 1509 GCACACATATATTTGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTTACACCGGTGGA 1568
 Qy 1753 TATTTACGGGAAAGCGTGTGCTGATGTTGCTCGCCGAGACCTTACTGTGCTGGGA 1812
 Db 1569 TATTTACGGGAAAGCGTGTGCTGATGTTGCTCGCCGAGACCTTACTGTGCTGGGA 1628
 Qy 1813 TGGTTCTGATGTTCTGCTATTTTCCACCTGCAAGAGAGCAGCAAGCAAGATAT 1872

Db 1629 TGGTTCTGCATGTTCTCGCTATTTCCTCCACTGCAAGAGACGCCAAGAGCAGCATAT 1688
QY 1873 AAGAAATGGAGACCCACTGACTCAGCTTTTACACCTTTACACCATGATTAATCACCATGGCCA 1932
Db 1689 AAGAAATGGAGACCCACTGACTCAGCTTTTACACCTTTACACCATGATTAATCACCATGGCCA 1748
QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGATAGTAGACATATTTTGGATGCG 1992
Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGATAGTAGACATATTTTGGATGCG 1808
QY 1993 TCCGAAGTCCGAGAGAGCCCTGGTCTATTGGCAATTTCCAGAGCGGAGAAATGAAGAGCGAAA 2052
Db 1809 TCCGAAGTCCGAGAGAGCCCTGGTCTATTGGCAATTTCCAGAGCGGAGAAATGAAGAGCGAAA 1868
QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCCTACGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCCTACGTAG 1928
QY 2113 TCTACAACAGAGGATTTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCTATACA 2172
Db 1929 TCTACAACAGAGGATTTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCTATACA 1988
QY 2173 AACTCTTCTTAAGGTAAACCTCGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTCTTCA 2232
Db 1989 AACTCTTCTTAAGGTAAACCTCGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTCTTCA 2048
QY 2233 TAAAGATGATGAGAGTGGCTCTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGAGAGTGGCTCTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2108
QY 2293 CAGAAGGTCTGGTACAGAGACTTCTATGAGCTCATCAACACCCCAATCTCAACACGAT 2352
Db 2109 CAGAAGGTCTGGTACAGAGACTTCTATGAGCTCATCAACACCCCAATCTCAACACGAT 2168
QY 2353 GGATGAGTTCTGTGAACAGTTTGGAAAGGGACCGAAACAACTGCGCAAGGCCAGG 2412
Db 2169 GGATGAGTTCTGTGAACAGTTTGGAAAGGGACCGAAACAACTGCGCAAGGCCAGG 2228
QY 2413 ACATACCCCGAGGACAGTAACAAATGGAAGCACCTTACAGAAATAAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGAGGACAGTAACAAATGGAAGCACCTTACAGAAATAAAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGCCACGAAATTTGAGAGGCCACCGAGAGTGTCTGAGCTGCAATACCTCTAGA 2532
Db 2289 CAGGAGGCCACGAAATTTGAGAGGCCACCGAGAGTGTCTGAGCTGCAATACCTCTAGA 2348
QY 2533 AACCTCAACAAAGTAGAATCTGCTAGACAATACTGGAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTAGAATCTGCTAGACAATACTGGAAACAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGGCATTTATGATGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACTTTTTCATGGCATTTATGATGATGTTTACAATGGTGGGAAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTAATAATTAATCAGATGAACTTCTCTAATAGGCTTTTTTTC 2702
Db 2469 CCAATTAATAATTAATCAGTAACTTCTCTAATAGGCTTTTTTTC 2518

RESULT 5

US-10-669-176-9
; Sequence 9, Application US/10669176
; Publication No. US20040214766A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: VEGF-C OR VEGF-D MATERIALS AND METHODS FOR TREATMENT OF
; FILE REFERENCE: 28967/37564B
; CURRENT APPLICATION NUMBER: US/10/669,176
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9

; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(2331)
US-10-669-176-9

Query Match 92.6%; Score 2508.4; DB 18; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGTTAACTAGGATGCTGTCTTTCTGGGAGTATTACTACAGC 252
Db 9 CTGAGCATGGCTGTTAACTAGGATGCTGTCTTTCTGGGAGTATTACTACAGC 68
QY 253 AAGAGCAAACTATCAGAATGGGAAGAACAATGTGCAAGGCTGAAATATCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAATGGGAAGAACAATGTGCAAGGCTGAAATATCTTACAAAGA 128
QY 313 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCA 372
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QY 433 TTTCTTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 492
Db 249 TTTCTTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATCAAGTGGGCTTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 552
Db 309 CAGAAGAGATGAATCAAGTGGGCTTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTCA 368
QY 553 CAAAGTACTTAAGGATTAATATCAGATCACTTTGTCGCTGTGGAACGCGGCTTTTCA 612
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Db 429 TCCAAATTTGCACTTCAATTTGAAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGA 488
QY 673 GAACTCACAATTTTGAAGACGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAG 732
Db 489 GAACTCACAATTTTGAAGACGCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAG 548
QY 733 ATCCCTTTTAATAGATGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAATAGATGAGAAATTAATCTCTGGAACCTGAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGCTATCTTCGAACTCTTTGGGACCCACCCCAATTCAGGACAGACGATGATTC 852
Db 609 CTTTGCTATCTTCGAACTCTTTGGGACCCACCCCAATTCAGGACAGACGATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTCCCAACCTCTCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTTAGTCCCAACCTCTCTCAGAGAGTGACAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTCGTGGAAATGCAATAGATGGAGAACACTCTCG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTCGTGGAAATGCAATAGATGGAGAACACTCTCG 788
QY 973 AAAAGTACTCAGCTAGATAGGTTGAGTATGCAAGTATGCTTTGGGGGACAGAG 1032
Db 789 AAAAGTACTCAGCTAGATAGGTTGAGTATGCAAGTATGCTTTGGGGGACAGAG 848
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Db 849 TCTGCTGAATAAATGGACAACTTCTCAAAGCTCGTCTGATTTGCTCAGTCCAGGCTCC 908
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Db 909 AAATGCAATGACACTCAITTTGATGAACCTGAGGATGATTCTTAATGAATTTAAAGA 968
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QY 1213 AGCCGTGTGTATGATATAGCATGATGATGAGAGGTTGTTCTTGGTCCATATGCCCCA 1272
Db 1029 AGCCGTGTGTATGATATAGCATGATGATGAGAGGTTGTTCTTGGTCCATATGCCCCA 1088
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Db 1089 CAGGGATGAGCCCAACTATCAATGAGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1148
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Db 1149 AGGAACCTTCCAGCAAAACATTTGGTGTGTTTGAATCTCAAGAGGACCTTCTGTATGA 1208
QY 1393 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTGTTTCTTATGAACA 1452
Db 1209 TGTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTGTTTCTTATGAACA 1268
QY 1453 TCGCCCAATAGTATCAAAACCGATGATAAATTTATCAAAATTTACAAAATTTGCTAGACCG 1512
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QY 1513 AGTGAATGAGAGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
Db 1329 AGTGAATGAGAGATGAGACATGATGATGATGATGATGATGATGATGATGATGATGATG 1388
QY 1573 TCTTAAAGTAGTTTCAATTTCTTAAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA 1632
Db 1389 TCTTAAAGTAGTTTCAATTTCTTAAAGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA 1448
QY 1633 AGAATGACAGTTTTTCGGGAACCGACTGCTATTTTTCAGCAATGAGAGCTTTTCCACTAAGA 1692
Db 1449 AGAATGACAGTTTTTCGGGAACCGACTGCTATTTTTCAGCAATGAGAGCTTTTCCACTAAGA 1508
QY 1693 GCAACAACTATATATTTGTTTCAACGCTGGGTTGCCAGCTCCCTTTACACCGTGTGA 1752
Db 1509 GCAACAACTATATATTTGTTTCAACGCTGGGTTGCCAGCTCCCTTTACACCGTGTGA 1568
QY 1753 TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTCTTGGGA 1812
Db 1569 TATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTCTTGGGA 1628
QY 1813 TGGTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATAT 1872
Db 1629 TGGTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATAT 1688
QY 1873 AAGAAATGAGACCCACTGACTCACTGTTTCAGACTTTACACCATGATATCACCATGGCCA 1932
Db 1689 AAGAAATGAGACCCACTGACTCACTGTTTCAGACTTTACACCATGATATCACCATGGCCA 1748
QY 1933 CAGCCCTGAAGAGAGAACTATCTATGTTGATAGAGAAATAGTAGCAATTTTGGAAATGAG 1992
Db 1749 CAGCCCTGAAGAGAGAACTATCTATGTTGATAGAGAAATAGTAGCAATTTTGGAAATGAG 1808
QY 1993 TCGGAAGTCGAGAGAGCGCTGCTATTTGGCAATTCAGAGCGCAATGAAGACGGA 2052
Db 1809 TCGGAAGTCGAGAGAGCGCTGCTATTTGGCAATTCAGAGCGCGAAATGAAGACGGA 1868
QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCCCTTCTGCTACGTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCCCTTCTGCTACGTAG 1928
QY 2113 TCTCAACAGAGAGATTCAGGCAATTAATCTCTGCAATGCGGTGGAAATGGTTTCAATACA 2172
Db 1929 TCTCAACAGAGAGATTCAGGCAATTAATCTCTGCAATGCGGTGGAAATGGTTTCAATACA 1988
QY 2173 AACTCTTCTTAAGGTAAACCTCGGAATCATTTGACACAGAGCATTTGGAGACCTTTTCA 2232

Db 1989 AACTCTTCTTAAGGTAAACCTCGGAAGTCAATTTGACACAGAGCATTTGGGAAGAACTTTTCA 2048
QY 2233 TAAAGATGATGATGAGATGCTCTTAAAGCAAAAGAAATGTCATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGATGCTCTTAAAGCAAAAGAAATGTCATAGCATGACACCTAG 2108
QY 2293 CCAGAAGGTCTGTTGATCAGAGACTTCATGCGAGCTCATCAACACCCCAATCTCAACACGAT 2352
Db 2109 CCAGAAGGTCTGTTGATCAGAGACTTCATGCGAGCTCATCAACACCCCAATCTCAACACGAT 2168
QY 2353 GGATGAGTCTGTTGATGAAAGTTGAAAGGAGCCGAAACAACTCGGCAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTTGATGAAAGTTGAAAGGAGCCGAAACAACTCGGCAAGGCCAGG 2228
QY 2413 ACATACCCCGGAGACGATTAACAAATGGAACACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGGAGACGATTAACAAATGGAACACTTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCACGAATTTGAGAGGACCCAGAGGAGTCTGAGCTGCATTTACCTCTAGA 2532
Db 2289 CAGGAGGACCCACGAATTTGAGAGGACCCAGAGGAGTCTGAGCTGCATTTACCTCTAGA 2348
QY 2533 AACCTCAAAAGTAGAAAACCTTGCCTAGACAATAAATGCAATATACAT 2592
Db 2349 AACCTCAAAAGTAGAAAACCTTGCCTAGACAATAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGCGCATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2652
Db 2409 GAACTTTTTCATGCGCATTTATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 2468
QY 2653 CCAATTAATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTTTTCC 2702
Db 2469 CCAATTAATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTTTTCC 2518

RESULT 6

US-10-723-860-2569
; Sequence 2569, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2569
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-2569

Query Match 92.6%; Score 2508.4; DB 18; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGACAGATGGGCTGTTAACTAGATTTGCTCTTTTCTGGGAGATTTACTTTACAGC 252
Db 9 CTGACAGATGGGCTGTTAACTAGATTTGCTCTTTTCTGGGAGATTTACTTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGAAGAAACAATGTGCAAGGCTGAAATTTCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGAAGAAACAATGTGCAAGGCTGAAATTTCTTACAAAGA 128
QY 313 AATGTGGAATCCCAACATGATGATCACTTTCAATGGCTTTGGCCACAGCTCCAGTTATCA 372
Db 129 AATGTGGAATCCCAACATGATGATCACTTTCAATGGCTTTGGCCACAGCTCCAGTTATCA 188

QY 373 TACCTTCCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
 Db 189 TACCTTCCCTTTTGGATGAGGAAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
 QY 433 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTCGCGAGTATCTTACAC 492
 Db 249 TTCAATTCGACCTGGTTAAATCAAGGATTTTCAAAAGATTTGTCGCGAGTATCTTACAC 308
 QY 493 CAGAAGAGATGAATCAAGTGGGCTGGAAGAGACATCTGAAAGATTTGCTAAATTTTCAT 552
 Db 309 CAGAAGAGATGAATCAAGTGGGCTGGAAGAGACATCTGAAAGATTTGCTAAATTTTCAT 368
 QY 553 CAAAGTACTTAAGGCATATAATCAGACTCACTTGTAGCCTGTGGAACCGGGGCTTTTCA 612
 Db 369 CAAAGTACTTAAGGCATATAATCAGACTCACTTGTAGCCTGTGGAACCGGGGCTTTTCA 428
 QY 613 TCCAAATTCGACCTCAATTTGAATTTGAGCATCATCTGAGGACAAATTTTAAAGCTGA 672
 Db 429 TCCAAATTCGACCTCAATTTGAATTTGAGCATCATCTGAGGACAAATTTTAAAGCTGA 488
 QY 673 GAACTCACATTTTGAAGACGGCGTGGGAGAGATCCATATGACCTTAAGCTGTGACAGC 732
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 QY 973 AAAAGTACTCAGCTAGATAGGTGAGATGCAAGATGACTTTGGAGGGGACAGAAAG 1032
 Db 789 AAAAGTACTCAGCTAGATAGGTGAGATGCAAGATGACTTTGGAGGGGACAGAAAG 848
 QY 1033 TCTGGTGAATAAATGACAAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCC 1092
 Db 849 TCTGGTGAATAAATGACAAACATTTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCC 908
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 Db 909 AAATGGCATTTGACACTCAATTTGATGAACTGCAGGATGATTTCTTAATGAACCTTTAAAGA 968
 QY 1153 TCCATAAATCCAGTTGTATAGGATGTTTACGACTTCCAGTAAACATTTTCAAGGGATC 1212
 Db 969 TCCATAAATCCAGTTGTATAGGATGTTTACGACTTCCAGTAAACATTTTCAAGGGATC 1028
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 Db 1029 AGCCGTGTGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATGCCCCA 1088
 QY 1273 CAGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGGC 1332
 Db 1089 CAGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGGC 1148
 QY 1333 AGGAATCTTCCAGCAAAACATTTGGTGTGTTGATCTCAAAAGGACCTTCTGTATGA 1392
 Db 1149 AGGAATCTTCCAGCAAAACATTTGGTGTGTTGATCTCAAAAGGACCTTCTGTATGA 1208
 QY 1393 TGTATAACCTTTGCAAGAGTCAATCCAGCATGTACAATCCAGTGTCTTCTATGAACA 1452
 Db 1209 TGTATAACCTTTGCAAGAGTCAATCCAGCATGTACAATCCAGTGTCTTCTATGAACA 1268

QY 1453 TCGCCCAATAGTATGATCAAAACGAGATGTAAATTTATCAATTTTACAAATTTGTCGTAGACCG 1512
 Db 1269 TCGCCCAATAGTATGATCAAAACGAGATGTAAATTTATCAATTTTACAAATTTGTCGTAGACCG 1328
 QY 1513 AGTGGATGCAGAAAGATGAGACGATGATGTTATGTTATCGGAAACAGATGTTGGGACCGT 1572
 Db 1329 AGTGGATGCAGAAAGATGAGACGATGATGTTATGTTATCGGAAACAGATGTTGGGACCGT 1388
 QY 1573 TCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGA 1632
 Db 1389 TCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAAAGAGGTTCTGCTGA 1448
 QY 1633 AGAAATGACAGTTTTTTCGGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTCCACTAAGCA 1692
 Db 1449 AGAAATGACAGTTTTTTCGGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508
 QY 1693 GCAACAACTATATATTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGGTGTA 1752
 Db 1509 GCAACAACTATATATTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACGGGTGTA 1568
 QY 1753 TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA 1812
 Db 1569 TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTTACTGTGCTTTGGGA 1628
 QY 1813 TGGTTCTGCATGTTCTGCTATTTTCCCACTGCAAAAGAGACGCAAAAGAGCAAGATAT 1872
 Db 1629 TGGTTCTGCATGTTCTGCTATTTTCCCACTGCAAAAGAGACGCAAAAGAGCAAGATAT 1688
 QY 1873 AAGAATGAGACCCCACTGACTCAGCTTTCAGACTTTACACCATGATAATCACCATGGCCA 1932
 Db 1689 AAGAATGAGACCCCACTGACTCAGCTTTCAGACTTTACACCATGATAATCACCATGGCCA 1748
 QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1992
 Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGGTGTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1808
 QY 1993 TCCGAAGTGCAGAGAGCGCTGCTATTTGGCAATTCAGAGCGGCAAAATGAAGAGCGAAA 2052
 Db 1809 TCCGAAGTGCAGAGAGCGCTGCTATTTGGCAATTCAGAGCGGCGAAATGAAGAGCGAAA 1868
 QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGCTAG 2112
 Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGCTAG 1928
 QY 2113 TCTCAACACAGAAAGATTCAAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACA 2172
 Db 1929 TCTCAACACAGAAAGATTCAAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACA 1988
 QY 2173 AAATCTTTTAAAGGTAAACCTCGGAAGTCAATTGACACAGAGCAATTTGGAAAGAACTTCTTCA 2232
 Db 1989 AAATCTTTTAAAGGTAAACCTCGGAAGTCAATTGACACAGAGCAATTTGGAAAGAACTTCTTCA 2048
 QY 2233 TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
 Db 2049 TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
 QY 2293 CCAGAAGGTCTGCTGACAGACTTTCATGAGCTCATCAACCCCACTTCTCAACACGAT 2352
 Db 2109 CCAGAAGGTCTGCTGACAGACTTTCATGAGCTCATCAACCCCACTTCTCAACACGAT 2168
 QY 2353 GGATGATTTCTGTGAACAAATTTTGGAAAGGGACCGAAACCAACGTCGCGCAAGGGCAGG 2412
 Db 2169 GGATGATTTCTGTGAACAAATTTTGGAAAGGGACCGAAACCAACGTCGCGCAAGGGCAGG 2228
 QY 2413 ACATACCCAGGAAACAGTAAACAAATTTGGAAGCACTTACAAAGAAATAAAGAAAGGTAGAAA 2472
 Db 2229 ACATACCCAGGAAACAGTAAACAAATTTGGAAGCACTTACAAAGAAATAAAGAAAGGTAGAAA 2288
 QY 2473 CAGGAGGACCCCAAGATTTTGAAGGGCACCCAGGAGTGTCTGAGCTGCAATTCCTCTAGA 2532
 Db 2289 CAGGAGGACCCCAAGATTTTGAAGGGCACCCAGGAGTGTCTGAGCTGCAATTCCTCTAGA 2348
 QY 2533 AACCTCAACAAAGTAGAATACTTGGCTTAGAATAAATCTGGAAACAAATGCAATATACAT 2592

Db 2349 AACCTCAACAGTAGAAGAACTTGCCTAGACAATAAAGTGGAAACAAATGCAATATACAT 2408
 QY 2593 GAACTTTTTCATGGCATTATGGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2652
 Db 2409 GAACTTTTTCATGGCATTATGGATGTTTCAATGGTGGGAAATTCAGCTGAGTTCCA 2468
 QY 2653 CCAATTATAAATAAATCCATAGTAGTAACCTTCCCTAATAGGCTTTTTTTTCC 2702
 Db 2469 CCAATTATAAATAAATCCATAGTAGTAACCTTCCCTAATAGGCTTTTTTTTTC 2518

RESULT 7

US-10-067-632-53
 : Sequence 53, Application US/10067632
 : Publication No. US20030166849A1
 : GENERAL INFORMATION:
 : APPLICANT: Goodman, Corey S.
 : Kolodkin, Alex L.
 : Matthes, David
 : Bentley, David R.
 : O'Connor, Timothy
 : TITLE OF INVENTION: The Semaphorin Gene Family
 : NUMBER OF SEQUENCES: 100
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 : STREET: 268 Bush Street, Suite 3200
 : CITY: San Francisco
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94104
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/10/067,632
 : FILING DATE: 04-Feb-2002
 : CLASSIFICATION: <Unknown>
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/09/060,610
 : FILING DATE: <Unknown>
 : APPLICATION NUMBER: 08/835,268
 : FILING DATE: <Unknown>
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Osman, Richard A.
 : REGISTRATION NUMBER: 36,627
 : REFERENCE/DOCKET NUMBER: B94-002-1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 343-4341
 : TELEFAX: (415) 343-4342
 : TELEX: <Unknown>
 : INFORMATION FOR SEQ ID NO: 53:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 2601 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: cDNA
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: 16..2331
 : SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-10-067-632-53
 Query Match 92.6%; Score 2508.4; DB 16; Length 2601;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 193 CTGCAGCATGGCTGGTTAACTAGGATTCGTCTCTTTCTGGGAGATTTACTTTACAGC 252
 Db 9 CTGCAGCATGGCTGGTTAACTAGGATTCGTCTCTTTCTGGGAGATTTACTTTACAGC 68

QY 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTGCAAGGCTGAAATTTATCTCTACAAAGA 312
 Db 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTGCAAGGCTGAAATTTATCTCTACAAAGA 128
 QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCA 372
 Db 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTTGGCCAAACAGCTCCAGTTATCA 188
 QY 373 TACCTTCTCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 432
 Db 189 TACCTTCTCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 248
 QY 433 TTTCAATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTTACAC 492
 Db 249 TTTCAATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTTACAC 308
 QY 493 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAT 552
 Db 309 CAGAAGAGATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCAT 368
 QY 553 CAGGTACTTTAAGGCATATATCAGACTCACTTTGTACGCTGTGGAACGGGGGCTTTTCA 612
 Db 369 CAGGTACTTTAAGGCATATATCAGACTCACTTTGTACGCTGTGGAACGGGGGCTTTTCA 428
 QY 613 TCCAAATTTGCACCTACTATTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGGA 672
 Db 429 TCCAAATTTGCACCTACTATTGAAATTTGGACATCATCTGAGGACATATATTTTAAAGCTGGA 488
 QY 673 GAACTCAATTTTGAAGACGGCGGTGGGAAGATCCATATGACCTTAAGTGTCTGACAGC 732
 Db 489 GAACTCAATTTTGAAGACGGCGGTGGGAAGATCCATATGACCTTAAGTGTCTGACAGC 548
 QY 733 ATCCCTTTTAAATAGATGAGAAATTTATCTCTGGAACCTGAGCTGATTTTATGGGGCGAGA 792
 Db 549 ATCCCTTTTAAATAGATGAGAAATTTATCTCTGGAACCTGAGCTGATTTTATGGGGCGAGA 608
 QY 793 CTTTGCTATCTTCCGAACTCTTTGGGCACACACCACCAATCAGGACAGAGCATGATTTC 852
 Db 609 CTTTGCTATCTTCCGAACTCTTTGGGCACACACCACCAATCAGGACAGAGCATGATTTC 668
 QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCTCAGAGAGTGAACAATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCACCTCATCTCTCAGAGAGTGAACAATCC 728
 QY 913 TGAAGATCACAAGATATATCTTTCTCCGTGAAATGCAATAGATGAGAGACACTCTGG 972
 Db 729 TGAAGATCACAAGATATATCTTTCTCCGTGAAATGCAATAGATGAGAGACACTCTGG 788
 QY 973 AAAAGCTACTCAACGCTAGATAGGTTCAGATATGCAAGAAATGACCTTTGGAGGGCAGAGAAG 1032
 Db 789 AAAAGCTACTCAACGCTAGATAGGTTCAGATATGCAAGAAATGACCTTTGGAGGGCAGAGAAG 848
 QY 1033 TCTGTTGAATTAATGGACAAACATTTCTCAAAAGCTGCTGTGATTTGCTCAGTGGCCAGGTCC 1092
 Db 849 TCTGTTGAATTAATGGACAAACATTTCTCAAAAGCTGCTGTGATTTGCTCAGTGGCCAGGTCC 908
 QY 1093 AAATGGCAATTCACACTCACTTTTGTATGAACTCGAGATGTTTCTTAATGAATTTTAAAGA 1152
 Db 909 AAATGGCAATTCACACTCACTTTTGTATGAACTCGAGATGTTTCTTAATGAATTTTAAAGA 968
 QY 1153 TCCTAAAAATCCAGTTGTATAGGAGTGTTCAGACTTTCCAGTAACTTTTCAAGGGATC 1212
 Db 969 TCCTAAAAATCCAGTTGTATAGGAGTGTTCAGACTTTCCAGTAACTTTTCAAGGGATC 1028
 QY 1213 AGCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTCCATATGCCCA 1272
 Db 1029 AGCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTCCATATGCCCA 1088
 QY 1273 CAGGATGGAGCCCAACTATCAATGGTGGCTTTATCAAGAAAGAGTCCCTTATCCACGGCC 1332
 Db 1089 CAGGATGGAGCCCAACTATCAATGGTGGCTTTATCAAGAAAGAGTCCCTTATCCACGGCC 1148

1333 AGGAACTGTCCTCCAGCAAAACATTTGGTGGTTTGAATCTCAAAAGGACCTTCTGTATCA 1392
 Db AGGAACTGTCCTCCAGCAAAACATTTGGTGGTTTGAATCTCAAAAGGACCTTCTGTATCA 1208
 1393 TGTATTAACCTTTGCAAGAGTCAATCCAGCAATGTACAATCAAGTGTCTTCTATGAACAA 1452
 Db TGTATTAACCTTTGCAAGAGTCAATCCAGCAATGTACAATCAAGTGTCTTCTATGAACAA 1268
 1453 TCGCCCAATAGTGATCAAAACCGATGTAAATATCAAAATTTACAAATTTGTCTGTAGACG 1512
 Db TCGCCCAATAGTGATCAAAACCGATGTAAATATCAAAATTTACAAATTTGTCTGTAGACG 1328
 1513 AGTGGATGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1572
 Db AGTGGATGAGAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1388
 1573 TCTTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATGATGATGATGATGATGATG 1632
 Db TCTTAAAGTGTGTTCAATTCCTAAGGAGACTTGGTATGATGATGATGATGATGATGATG 1448
 1633 AGAAATGACAGTGTTCGGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1692
 Db AGAAATGACAGTGTTCGGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCA 1508
 1693 GCAACAACTATATATTTGTTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACGGTGTGA 1752
 Db GCAACAACTATATATTTGTTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACGGTGTGA 1568
 1753 TATTTACGGGAAAGCTGTGCTGAGTGTGCTTCCGCGAGACCTTACTGTCTTGGGA 1812
 Db TATTTACGGGAAAGCTGTGCTGAGTGTGCTTCCGCGAGACCTTACTGTCTTGGGA 1628
 1813 TGGTTCGTGATGTTCTGCTATTTTCCCACTGCAAGAGACGCAACGACGACGACATAT 1872
 Db TGGTTCGTGATGTTCTGCTATTTTCCCACTGCAAGAGACGCAACGACGACGACATAT 1688
 1873 AAGAAATGAGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1932
 Db AAGAAATGAGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1748
 1933 CAGCCTGAAGAGAGAACTATCTATGCTGTAGAGATAGTACATATTTTGGAAATGCA 1992
 Db CAGCCTGAAGAGAGAACTATCTATGCTGTAGAGATAGTACATATTTTGGAAATGCA 1808
 1993 TCCGAAGTCCGAGAGAGCTGCTGCTATTTGGCAATTCAGAGCGCAAAATGAAGAGCGAAA 2052
 Db TCCGAAGTCCGAGAGAGCTGCTGCTATTTGGCAATTCAGAGCGCGAAATGAAGAGCGAAA 1868
 2053 AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCTTCTGCTAGCTAG 2112
 Db AGAAGAGATCAGAGTGGATGATCATATCATAGGACAGATCAAGGCTTCTGCTAGCTAG 1928
 2113 TCTCAACAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGACATGGGTTTATACA 2172
 Db TCTCAACAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGACATGGGTTTATACA 1988
 1929 TCTCAACAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGACATGGGTTTATACA 2048
 2173 AACTCTTCTTAAGGTAACCTCGAAGTCAATGACACAGAGCATTTGGAAAGAACTTCTTCA 2232
 Db AACTCTTCTTAAGGTAACCTCGAAGTCAATGACACAGAGCATTTGGAAAGAACTTCTTCA 2048
 2233 TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGATGACACCTAG 2292
 Db TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGATGACACCTAG 2108
 2293 CCAGAGGCTTGGTACAGAGATTCATGAGCTCATCAACACCCCACTCAACAGAT 2352
 Db CCAGAGGCTTGGTACAGAGATTCATGAGCTCATCAACACCCCACTCAACAGAT 2168
 2353 GGATGAGTTCGTGAAACAGTTTGGAAAGGAGACCGAAACCAACGTCGGCAAGGCGAGG 2412
 Db GGATGAGTTCGTGAAACAGTTTGGAAAGGAGACCGAAACCAACGTCGGCAAGGCGAGG 2228
 2413 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCACTTTTCAAGAAATAAGAAAGGTAGAAA 2472

2229 ACATACCCCGAGGAAACAGTAAACAAATGGAAGCCTTTACAGAAATAAGAAAGGTAGAAA 2288
 QY CAGGAGGACCCACGAAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCAATACCTCTAGA 2532
 Db CAGGAGGACCCACGAAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCAATACCTCTAGA 2348
 2533 AACCTCAACAAAGTGAAGAACTTGCCTAGACAATACTGGAAGAAACAAATGCAATATACAT 2592
 Db AACCTCAACAAAGTGAAGAACTTGCCTAGACAATACTGGAAGAAACAAATGCAATATACAT 2408
 2593 GAACTTTTTCATGTCATTTATGTCATGATGTTTCAATGTCGGAAGAAATTCAGCTGAGTTCCA 2652
 Db GAACTTTTTCATGTCATTTATGTCATGATGTTTCAATGTCGGAAGAAATTCAGCTGAGTTCCA 2468
 2653 CCAATTAATAAATAAATCCATGAGTAACTTTCCTAATAGCTTTTTTTTCC 2702
 Db CCAATTAATAAATAAATCCATGAGTAACTTTCCTAATAGCTTTTTTTTCC 2518

RESULT 8
 US-10-723-860-6714
 ; Sequence 6714, Application US/10723860
 ; Publication No. US20040253606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aziz, Natasha
 ; APPLICANT: Ginsburg, Wendy M.
 ; APPLICANT: Zlotnik, Albert
 ; TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions &
 ; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
 ; FILE REFERENCE: 05882.0193.NPUS01
 ; CURRENT APPLICATION NUMBER: US/10723,860
 ; CURRENT FILING DATE: 2003-11-26
 ; PRIOR APPLICATION NUMBER: 60/429,739
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 8393
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6714
 ; LENGTH: 3023
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-723-860-6714

Query: Match 92.6%; Score 2508.4; DB 18; Length 3023;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTGCAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGAGTATTACTTACAGC 252
 Db 9 CTGCAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGAGTATTACTTACAGC 68
 QY 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTCGAAGCTGAAATATCTTACAAAGA 312
 Db 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGTCGAAGCTGAAATATCTTACAAAGA 128
 QY 313 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
 Db 129 AATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188
 QY 373 TACCTTCTCTTTGGATGAGGAACGGATAGGCTGTATGTTGGAGCAAGGATCACATATT 432
 Db 189 TACCTTCTCTTTGGATGAGGAACGGATAGGCTGTATGTTGGAGCAAGGATCACATATT 248
 QY 433 TTTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC 492
 Db 249 TTTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC 308
 QY 493 CAGAAGAGATGAATCAAGTGGCTGGAAGACATCTCTGAAAGAAATGTGCTAAATTTCAAT 552
 Db 309 CAGAAGAGATGAATCAAGTGGCTGGAAGACATCTCTGAAAGAAATGTGCTAAATTTCAAT 368
 QY 553 CAGGTACTTAAAGCATATATATCAGATCCTTGTACGCTGTGGACCGGGGCTTTTCA 612

Db	369	CAAGGTACTTAAAGGCATATAATCAGACTCATCTGTAGCCCTGTGGAAACGGGGCGCTTTTCA	428
Qy	613	TCCAAATTTGCACCTACATATTGAAATTTGGACATCATCTCTGAGGACAATAATTTTTTAAGCTGGGA	672
Db	429	TCCAAATTTGCACCTACATATTGAAATTTGGACATCATCTCTGAGGACAATAATTTTTTAAGCTGGGA	488
Qy	673	GAACTCACATTTTTGAAAACGGCCGTGGGAAGAGTCCCATATGACCCTTAAGCTGTGTGACAGC	732
Db	489	GAACTCACATTTTTGAAAACGGCCGTGGGAAGAGTCCCATATGACCCTTAAGCTGTGTGACAGC	548
Qy	733	ATCCCTTTTAATAGATGAGAAATTTATACTCTGTGAAATCTGCAGCTGATTTTTATGGGGCGAGA	792
Db	549	ATCCCTTTTAATAGATGAGAAATTTATACTCTGTGAAATCTGCAGCTGATTTTTATGGGGCGAGA	608
Qy	793	CTTTGTCTATCTTCCGAACCTCTTGGGCAACCAACCCAAATCAGGACAGAGCATGATTC	852
Db	609	CTTTGTCTATCTTCCGAACCTCTTGGGCAACCAACCCAAATCAGGACAGAGCATGATTC	668
Qy	853	CAGGTGGCTCAATGATCAAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAATCC	912
Db	669	CAGGTGGCTCAATGATCAAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAATCC	728
Qy	913	TGAAGATGACAAAGTATATCTTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTGG	972
Db	729	TGAAGATGACAAAGTATATCTTTTTCTTCCGTGAAATGCAATAGATGGAGAACACTCTGG	788
Qy	973	AAAAGCTACTCACCTAGATAGTGCAGATATGCAAGAATGACTTTGGAGGGCACAGAAG	1032
Db	789	AAAAGCTACTCACCTAGATAGTGCAGATATGCAAGAATGACTTTGGAGGGCACAGAAG	848
Qy	1033	TCTGGTGAATAAAATGGGACAACTTCTCAAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	1092
Db	849	TCTGGTGAATAAAATGGGACAACTTCTCAAAGCTCGTCTGATTTGCTCAGTGCACAGTCC	908
Qy	1093	AAATGGCAATTGACACTCATTTTTGATGAATCGCAGGATGTATTCCTAATGAACCTTTAAAGA	1152
Db	909	AAATGGCAATTGACACTCATTTTTGATGAATCGCAGGATGTATTCCTAATGAACCTTTAAAGA	968
Qy	1153	TCCTAAAAATCCAGTGTGTATGAGTGTTTACGACTTCCAGTAAACAATTTTCAAGGGATC	1212
Db	969	TCCTAAAAATCCAGTGTGTATGAGTGTTTACGACTTCCAGTAAACAATTTTCAAGGGATC	1028
Qy	1213	AGCCGTGTGTATGATAGCATGATGATGAGAAAGGTGTCTCTTGGTCCATATGCCCA	1272
Db	1029	AGCCGTGTGTATGATAGCATGATGATGAGAAAGGTGTCTCTTGGTCCATATGCCCA	1088
Qy	1273	CAGGGATGGACCCAACTCATCAATGGGTGCCTTATCAAGGAAGAGTCCCTCTATCCAGGGC	1332
Db	1089	CAGGGATGGACCCAACTCATCAATGGGTGCCTTATCAAGGAAGAGTCCCTCTATCCAGGGC	1148
Qy	1333	AGGAACTTGTCCCAAGCAAAACATTTGGTGGTGTTTGACTCTACAAAGACCTTCTCTGATGA	1392
Db	1149	AGGAACTTGTCCCAAGCAAAACATTTGGTGGTGTTTGACTCTACAAAGACCTTCTCTGATGA	1208
Qy	1393	TGTTTAAACCTTTGCAAGAAGTCAATCAGCCATGTACAATCCAGTGTTCCTATGAACAA	1452
Db	1209	TGTTTAAACCTTTGCAAGAAGTCAATCAGCCATGTACAATCCAGTGTTCCTATGAACAA	1268
Qy	1453	TCGCCCAATAGTGAATCAAAACGGATGTAAATTTATCAATTTACAAATTTGCTGTAGACCG	1512
Db	1269	TCGCCCAATAGTGAATCAAAACGGATGTAAATTTATCAATTTACAAATTTGCTGTAGACCG	1328
Qy	1513	AGTGGATGCAAGATGGACAGTATGATGTATGTTTTATCGGAACAGATGTTGGGACCGT	1572
Db	1329	AGTGGATGCAAGATGGACAGTATGATGTATGTTTTATCGGAACAGATGTTGGGACCGT	1388
Qy	1573	TCCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAAAGAGAGTCTCTGTGGA	1632
Db	1389	TCCTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAAAGAGAGTCTCTGTGGA	1448
Qy	1633	AGAAATGACAGTTTTTTCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCA	1692
Db	1449	AGAAATGACAGTTTTTTCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTTCCACTAAGCA	1508

QY	1693	GCACAACTATATATATTTGGTTTCAACGCGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGA	1752
DB	1509	GCACAACACTATATATTTGGTTTCAACGCGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGA	1568
QY	1753	TATTTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGAGCCCTTACTGTGCTTCGGGA	1812
DB	1569	TATTTTACGGGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGAGCCCTTACTGTGCTTCGGGA	1628
QY	1813	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCGAAAGAGACGCAACAAGATAT	1872
DB	1629	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCGAAAGAGACGCAACAAGATAT	1688
QY	1873	AAGAAATGAGACCCACTGCACTCACTGTTCAGACTTACACCATGATAATCACCATGSCCA	1932
DB	1689	AAGAAATGAGACCCACTGCACTCACTGTTCAGACTTACACCATGATAATCACCATGSCCA	1748
QY	1933	CAGCCCTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCACATTTTTGGAATGCAG	1992
DB	1749	CAGCCCTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCACATTTTTGGAATGCAG	1808
QY	1993	TCCGAAGTCGACAGAGAGCGCTGCTTATTTGGCAATTCAGAGGCGGAAATCGAAGCGGAAA	2052
DB	1809	TCCGAAGTCGACAGAGAGCGCTGCTTATTTGGCAATTCAGAGGCGGAAATCGAAGCGGAAA	1868
QY	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	2112
DB	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	1928
QY	2113	TCTACAAACAGAGAGGATTCAGGCAATTTACCTCTGCGCATCGGTGGAAACATGGGTTTATACA	2172
DB	1929	TCTACAAACAGAGAGGATTCAGGCAATTTACCTCTGCGCATCGGTGGAAACATGGGTTTATACA	1988
QY	2173	AACCTCTTTAAGGTAAACCTGGAGATCATGACACAGAGCAATTTGGAAAGAACTTCTTCA	2232
DB	1989	AACCTCTTTAAGGTAAACCTGGAGATCATGACACAGAGCAATTTGGAAAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGATGAGATGGCTCTTAAGACACAAAGAAATGTCCAAATAGCATGACACCTAG	2292
DB	2049	TAAAGATGATGATGAGATGGCTCTTAAGACACAAAGAAATGTCCAAATAGCATGACACCTAG	2108
QY	2293	CCAGAAGCTGTGGTACAGAGACTTCAATGAGCTCATCAACCCCAATCTTCAACACGAT	2352
DB	2109	CCAGAAGCTGTGGTACAGAGACTTCAATGAGCTCATCAACCCCAATCTTCAACACGAT	2168
QY	2353	GGATCAGTCTTGTAACAAAGTTTGGAAAGGGACCGAAACAAACGTCGCGCAAGGCCGAGG	2412
DB	2169	GGATCAGTCTTGTAACAAAGTTTGGAAAGGGACCGAAACAAACGTCGCGCAAGGCCGAGG	2228
QY	2413	ACATACCCCGGGAAACAGTAAACAAATGGAGACATTTACAAGAAAAATAGAAAGGTAGAAA	2472
DB	2229	ACATACCCCGGGAAACAGTAAACAAATGGAGACATTTACAAGAAAAATAGAAAGGTAGAAA	2288
QY	2473	CAGGAGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACTCTTAGA	2532
DB	2289	CAGGAGGACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTCTGAGCTGCATTACTCTTAGA	2348
QY	2533	AACCTCAAAACAGTAGAAACTTGCCTAGACAAATAACTGGAAAAACAAATGCAATATACAT	2592
DB	2349	AACCTCAAAACAGTAGAAACTTGCCTAGACAAATAACTGGAAAAACAAATGCAATATACAT	2408
QY	2593	GAACTTTTTTTCATGCGCATATGTGTGATGTTTACAATGTGGGAAATTCAGCTCAGTTCGA	2652
DB	2409	GAACTTTTTTTCATGCGCATATGTGTGATGTTTACAATGTGGGAAATTCAGCTCAGTTCGA	2468
QY	2653	CCAAATATAAATTAATCCATGAGTAACATTTCCCTAATAGGCTTTTTTTTCC	2702
DB	2469	CCAAATATAAATTAATCCATGAGTAACATTTCCCTAATAGGCTTTTTTTTTC	2518

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; Publication No. US20030232411A1
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE THEREOF
; FILE REFERENCE: Q59878
; CURRENT APPLICATION NUMBER: US/10/404,438
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/582,419A
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05952
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: P. Hei. 9-358811
; PRIOR FILING DATE: 1997-12-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-404-438-2

Query Match      26.5%; Score 718.6; DB 17; Length 2331;
Best Local Similarity 61.9%; Pred. No. 1.2e-202;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY      269 AATGGGAAGAACATGTGCGCAAGGCTGAAATATCTACAAAGAAATGTTGGAATCCAAC 328
DB      109 ACTTTGAAGCAAAATATTCAGAGACTCAAGCTAACTACAAAGACTTGTGCTCTTCAAT 168

QY      329 AATGTGATCATTTCATGGCTTGGCCACAGCTCCAGTATCATACCTTCTTTTGGAT 388
DB      169 ACCTGTATTCCCTTTTGGGTTTCATCAGAGGACTGGATTTTCAAACTCTCTCTTAGAT 228

QY      389 GAGGAACGAGTAGGCTGTATGTGGAGCAAGAGATCACATATTTTCATTCGACCTGGTT 448
DB      229 GAGGAAGGCGAGGCTGCTCTTGGAGCCAAAGACCACATCTTCTACTCAGTCTGGTT 288

QY      449 AA---TATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACACCAAGAGAGATGAA 505
DB      289 GACTTTAAACAAAATTTTAAAGATTTTATGGCTGCTGCAAGCGGCTGGAATTA 348

QY      506 TCCAAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAAATTTTCATCAGTACTTAAG 565
DB      349 TGTAAATTAGCTGGGAAGATGCCAATACAGATGTGCAATTTTCATCAGAGTACTTCAG 408

QY      566 GCATATAATCAGACTCACCTTGAGCCTGTGGAACGGGGCTTTTCATCCAATTTGCAACC 625
DB      409 CCTATTAACAAATCTCACATATATGTGTGGAACCTGGAGCAATTTCAATCAATATGTGG 468

QY      626 TACATTGAAATTTGGACATCATCTCGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT 685
DB      469 TATATTGATCTTGGAGCTACAAGGAGGATATTATATTCAAACTAGACACAGCTAATTTG 528

QY      686 GAAACGGCGCTGGGAAGAGTCCATATGACCCCTAGAGTCTGACAGCATCCCTTTTAATA 745
DB      529 GAGTCTGGCAGACTGAAATGTCTTTCGATCTCTCAGAGCCTTTTGTCTTCAATATGACA 588

QY      746 GATGAGATTTACTCTCGAACTGACGCTGATTTTATGGGGGAGAGACTTTGCTATCTTC 805
DB      589 GATGAGTACCTTACTCTGGAACAGCTTCTGATTTCTTGGCAAGATACCTGATCTACT 648

QY      806 CGAACTCTTGGGC-----ACCACCAACCAATCAGGACAGAGCAGCATGATTTCCAGG 856
DB      649 CGATCCCTTGGGCTTACTCATGCCACCACTACATCAGAACTGACATTTTCAGAGCACTAC 708

QY      857 TGGCTCAATGATCCAAAGTTCAATATGATGCGCCACCTCATCTCAGAGAGTACAAATCTGAA 916
DB      709 TGGCTCAATGAGGCAAAATTTATTTGAACTTTCTTTCATACCAACAGACACCTTCAATCCAGAT 768

QY      917 GATGACAAAGTACTTTTCTTCGTGAAATGCAATAGATGGAGACACTCTGGAATA 976
DB      769 GATGATAAAATATATTTCTTCTTCTCGTGAATCATCTCAAGAGGCGAGTACCTCCGATAAA 828

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QY      977 GCTACTCAGCTAGTAATAGTTCAGATATGCAAGATAGACTTTTGGAGGGCAGCAAGAGTCTG 1036
DB      829 ACCATCTCTTCTCGAGTTTGAAGAGTTTGTAAAGATATGATGAGGAGCAACGCGACCTTG 888

QY      1037 GTGAATAAATGGACAACATCTCTCAAGCTCGTCTGATTTTGTCTAGTCCAGTCCCAAT 1096
DB      889 ATAAACAAGTGGACGACCTTTCTTAAGCCAGACTGATTTGCTCAATTTCTTGGAAAGTAT 948

QY      1097 GGCATTGACACTCATTTTGTGAACTGCAGGAGTATTTCTTAATGAACCTTTTAAAGATCT 1156
DB      949 GGGGAGATATCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1008

QY      1157 AAAAATCCAGTTGATATATGAGTGTTTAGGACTTCCAGTAAACATTTTCAAGGAGTACGC 1216
DB      1009 AGAAATCTGTAGTATATGAGTCTTTTACTCAACAGCTCCATCTTCAAGGCTCTGCT 1068

QY      1217 GTGTGTATGTATAGCATGATGATGAGAGGGTGTCTTGGTCCATATATCCACACAGG 1276
DB      1069 GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAG 1128

QY      1277 GATGACCCCACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTATTCACGGCCAGGA 1336
DB      1129 GAAAGTCAGACCATCTGTTGGGTGAGTATGATGGAGAAATTTCTTATCCACGGCTGCT 1188

QY      1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTGTACTCTAAGAGACCTTCTCTGATGAT 1393
DB      1189 ACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1248

QY      1394 GTTATAACCTTTGCAAGAAAGTCAATCCAGCCATGTAACAATCCAGTGTTCCTATGAACAAT 1453
DB      1249 GTCATCAGTTTCATTAAGGGGCACTCTGTGATGTATAAGTCCGTATATCCAGTTGACAGA 1308

QY      1454 CGCCCAATAGTGATCAAAACCGGATGTAAATTTATCAATTTTACACAAATTTGTCTGTAGACC 1513
DB      1309 GGACCAACGTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGTGGATCAT 1368

QY      1514 GTGAGTACGAAAGATGAGCAGTATGATGTTTATCGGAACAGAGATGTTGGGACCGTT 1573
DB      1369 GTCAATTGCAAGAGATGGCCAGTACGATGTAATGTTTCTTGGAAACAGACATTTGGAAC 1428

QY      1574 CTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAAAGAGAGTCTTCTGCTG 1633
DB      1429 CTCAAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGTAGTGTCTGGAG 1485

QY      1634 GAAATGACAGATTTTTCGGGAACCGGACTGCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCAG 1693
DB      1486 GAGTTGACAGATTTTCAAGCACTCATCAATCATCTTTGAACATGGAATTTGTCTCTGAAGCAG 1545

QY      1694 CAACAACTATATATTTGTTTCAACGGCTGGGTTGCCAGTCTCCCTTTTACACCGGTGTGAT 1753
DB      1546 CAACAAATTTGATATTTGTTTCCGAGATGGAATTTAGTTTCACTCTCTCTTGCACAGATGCGAC 1605

QY      1754 ATTTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGAGCCCTTACTGCTCTGGGAT 1813
DB      1606 ACTTATGGGAAGCTTGGCAGACTGTTGTCTTTCGAGAGACCCCTTACTGTGCTCTGGGAT 1665

QY      1814 GGTTCCTGATGTTTCTGCTATTTTCCCACTGCAAGAGAGACGCAAGAGCAAGATATA 1873
DB      1666 GGAATGATGCTCTCTGATATGCTCTACTTCTTAAGAGAGAGCTAGACGCCAAGATGTA 1725

QY      1874 AGAAATGAGAGCCCACTGACTCATCTGTTTCAAGATTTTACCATGATAATCCATGCGCAC 1933
DB      1726 AAATATGCGGACCAATCAACAGTGTGGGACATCGAAGACAGCATAGTATGATG---AA 1782

QY      1934 AGCCCTGAAGAGAGAGATCATCTATGTTGATAGAAATAGTAGACATTTTGGAAATGCACT 1993
DB      1783 ACTGCTGATGAAAGAGTGAATTTTGGCAATTTTAACTCAACCTTCTTGGAAATGATA 1842

QY      1994 CGGAAGTCCGAGAGAGCGCTGCTGTTTATTTGGCAATTTTCCAGAGGCGGAAATGAAGAGCGAAA 2053
DB      1843 CCTAAATCCCAACAGCAACTATTTAAATGGTATATCCAGAGGTGAGGGATGAGCATCGA 1902

QY      2054 GAAGAGATCAGAGTGGATGATCATATCATATCAGGACAGATCAAGGCGCTTCTGCTACGTAGT 2113

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Db 1903 GAGGAGTTGAGCCCGATGAAGAAATCATCAAAACCGAATATGGGTACTGATTCGAAT 1962
Qy 2114 CTACACAGAGGATTCAGCAATTAACCTGTGCCATGCGGTGGAAACATGGGTTTACATAA 2173
Db 1963 TTGCAGAGAAGGATTTCTGGGATGTATTACTGCAAAAGCCGAGGACACACTTTTCATCCAC 2022
Qy 2174 ACTCTTCTTAAGTAACCTGGAAGTCATTGACACAGAGCATTTGGAAGAACTTCTTCAT 2233
Db 2023 ACCATAGTGAAGTGAATTTGAATGTTCATGATGAACAGATGGAAATATCCAGAGG 2082
Qy 2234 AAAGATGATGATG 2246
Db 2083 GCAGAGCATGAGG 2095
RESULT 10
US-09-946-374-309
; Sequence 309, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Wickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
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; PRIOR APPLICATION NUMBER: 60/105807

Query Match      26.5%; Score 718.6; DB 10; Length 3871;
Best Local Similarity 61.9%; Pred. No. 1.6e-202;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTACAAAGAAATGTTGGAATCCAAAC 328
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QY 329 AATGTGATCATTCTTCAATGGCTTGGCCCAACAGCTCCAGTGTATCATACCTTCTTTTGGAT 388
DB 275 AGCTGATTTCCCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACACTCTTCTCTTAGAT 334
QY 389 GAGGAACGAGTAGCTGTATGTTGGAGCAAGAGTACATATTTTTCATTTCACCTGTT 448
DB 335 GAGGAAAGAGGAGGCTGCTCTTGGGAGCCAAAGACCAATCTTCTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTTACACAGAAGAGATGAA 505
DB 395 GACTTAAACAAAATTTTAAAGAGATTTATGGCCCTGTGCAAGAGGAGGTTGGAATTA 454
QY 506 TCGAAGTGGGCTGGAAAAGACATCTGAAAGAAATGTCTAAATTTTCATCAAGGTACTTAAG 565
DB 455 TGTAAATTTAGCTGGGAAAGATGCCAAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAG 514
QY 566 GCATATATCAGACTCATTGTACCCCTGTGGAACGGGGCTTTTCATCCCAATTTTGCACC 525
DB 515 CCCTATAACAAAACCTCACAATATATGTGTGGAACCTGGAGCATTTTCATCCCAATATGTGGG 574
QY 626 TACATTGAAATTTGGACATCATCTCAGGACATATATTTTAACTCGAGAGACTCACAATTTT 685
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QY 686 GAAAACGGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTCTGACAGCATCCCTTTTAATA 745
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DB 815 TGGCTCAATGGAGCAAAATTTTATGGAACCTTCTTCATACACAGACACCTTCAATCCAGAT 874
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DB 995 ATAAACAAGTGGAGCGACTTTTCTTAAGCCAGACTGATTTGCTCAATTCCTGGAAGTAT 1054
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DB 1115 AGAAATCCTGTAGTATATGGAGTCTTTTACTACAAACAGCTCATCTTCAAGGCTCTGCT 1174
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DB 1175 GTTGTGTGTATAGCATGAGTGTGTGAGAGGGTGTCTTGGTCCATATATGCTCATAG 1234
QY 1277 GATGACCCCAACTATCAATGGGTGCTTTATCAAGGAAGAGTCCCTTATCCACGGCAGGA 1336
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Db 1235 GAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAATTCCTTATCCAGCGCTGCT 1294
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 Db 1295 ACATGTTCCAGCAAAACCTTATGACCCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
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 Db 1832 AAATATGGCGACCAATCAACAGTGTCTGGGACATCGAAGACAGCATTAGTATG---AA 1888
 QY 1934 AGCCCTGAAGAGAGATCATCTATGTTGTAGAGAATAGTAGACATTTTGGAAATGCAAT 1993
 Db 1889 ACTGCTGATGAAAGTGAATTTTGGCATTTGAATTTAACTCAACCTTCTGGAATGTATA 1948
 QY 1994 CCGAATGCGCAGAGCGGTGCTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA 2053
 Db 1949 CCTAAATCCCAACAAGCACTATTAAATGGTATATCCAGAGTCAAGGATGAGCATCGA 2008
 QY 2054 GAAGATCAGAGTGGATGATCATATCATCGACAGATCAAGGCTTCTGCTAGTATG 2113
 Db 2009 GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAATG 2068
 QY 2114 CTCAACAGAGGATTCAGGCAATTAACCTCTGCCATGGGTGGAACATGGGTTTACACAA 2173
 Db 2069 TTGCAGAGAAGATTTCTGGGATGTTTACTGCAAGCCAGGAGCAGACATTTTCAATCAC 2128
 QY 2174 ACTTCTTAAGGTAAACCTTGAAGTCAATTTGACAGAGCATTTTGGAAAGAACTTCTTCA 2233
 Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCATTGAGATGAACAGATGGAATAATCCAGAGG 2188
 QY 2234 AAAGATGATG 2246
 Db 2189 GCAGAGCATGAGG 2201

RESULT 11
 US-10-052-586-347
 ; Sequence 347, Application US/10052586
 ; Publication No. US200201275841
 ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C1
 ; CURRENT FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
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 ; PRIOR FILING DATE: 1997-10-28
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 ; PRIOR APPLICATION NUMBER: 60/063564
 ; PRIOR FILING DATE: 1997-10-28
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 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063870
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/064103
 ; PRIOR FILING DATE: 1997-10-31
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066120
 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/066466
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/066772
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 ; PRIOR FILING DATE: 1997-12-11
 ; PRIOR APPLICATION NUMBER: 60/069425
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 ; PRIOR APPLICATION NUMBER: 60/069870
 ; PRIOR FILING DATE: 1997-12-17
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 ; PRIOR FILING DATE: 1997-12-18
 ; PRIOR APPLICATION NUMBER: 60/077450
 ; PRIOR FILING DATE: 1998-03-10
 ; PRIOR APPLICATION NUMBER: 60/077632
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/077649
 ; PRIOR FILING DATE: 1998-03-11
 ; PRIOR APPLICATION NUMBER: 60/078886
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/078939
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/079664
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079786
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;; PRIOR FILING DATE: 1998-03-31
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;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080333
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/081049
;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR FILING DATE: 1998-04-08
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;; PRIOR FILING DATE: 1998-06-04
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;; PRIOR FILING DATE: 1998-06-12
;; PRIOR APPLICATION NUMBER: 60/089512
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089514
;; PRIOR FILING DATE: 1998-06-16
;; PRIOR APPLICATION NUMBER: 60/089538
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089598
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089653
;; PRIOR FILING DATE: 1998-06-17
;; PRIOR APPLICATION NUMBER: 60/089908

Query Match 26.5%; Score 718.6; DB 13; Length 3871;

Best Local Similarity 61.9%; Pred. No. 1.6e-202; Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGAACAAATGTGCCAAGGCTGAAATATCTACAAAGAAATGTTCGAATCCAAC 328
DB 215 ACTTTGAAGCAAAATATTTCCAAGACTCAAGCTTAACCTCAAGAGACTTGCTGCTTTCAAT 274
QY 329 AATGTGATCATTTCATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTTTTGGAT 388
DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACTCTTCTCTTAGAT 334
QY 389 GAGGAACGAGTAGGCTGTATGTTGGCAAGAGATCATATTTTCATTCGACCTGGTT 448
DB 335 GAGGAAGAGGCAGGCTGCTCTTGGAGCCAAAGACCACATCTTCTTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAA 505
DB 395 GACTTAACAAAATTTTAAGAGATTTATTGGCTGCTGCAAGAGACGGGTGGNATTA 454
QY 506 TCGAAGTGGGCTGGAAAAGACATCTTGAAAGAAATGTGCTTAATTTTCATCAAGGTACTTAAG 565

Db 455 TGTAAATAGCTGGAAAGATGCAATACAGAATGTCAAATTTTCATCAGAGTACTTCAG 514
 QY 566 GCATATAATCAGACTCAGTTGTAGCGCTGTGGAAACGGGGCTTTTCATCCAAATTTGCACC 625
 Db 515 CCTTATAACAAACTCACATATATGTGTGGAACTGGAGCAATTCATCCAAATATGGG 574
 QY 626 TACATTTGAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTT 685
 Db 575 TATATTGATCTTGGAGCTACAGAGGAGATATATATTCAAAGTACACACATATTTG 634
 QY 686 GAAACCGCGCTGGGAGAGTCCATATGAGCCCTTAAGCTGTGACAGCATCCCTTTTAAATA 745
 Db 635 GAGTCTGGCAGACTGAAATGTCTTTTCGATCTCTCAGCAGCTTTTTCGTTTTCAGTAATGACA 694
 QY 746 GATGGAGAAATATACCTCTGGAATCTGAGCTGATTTTATGGGGGAGACTTTGCTATCTTC 805
 Db 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTTGGCAAGATATCTGATTTCACT 754
 QY 806 CGAACTCTTTGGG- - - - - ACCACCAACCAATCAGGACAGAGCATGATTTCCAGG 856
 Db 755 CGATCCTTTGGGCTACTCATGACCAACCACTACATCAGAACTGACATTTTCAGAGCACTAC 814
 QY 857 TGGCTCAATGATCCAAAGTTTATAGTGCACCTCATCTCAGAGAGTGAACAATCTCTGAA 916
 Db 815 TGGCTCAATGGAGCAAAATTTATTTGAACTTTTCTCATACAGACACCTTACAACTCCAGAT 874
 QY 917 GATGACAAAGTATACCTTTCTTCGTTGAAATGCAATAGATGGAGAACACTCTCGAAA 976
 Db 875 GATGATAAATATATTTCTTTCTTCTGTAATCATCTCAAGAAGGCGATGACCTCCGATAAA 934
 QY 977 GCTACTCAGCTAGAAATAGTGTAGATATGCAAGAAATGACTTTGGAGGGCAGACAAAGTCTG 1036
 Db 935 ACCATCTTTCTCGAGTTGGAAGAGTTTCTAAGAAATGATGAGGAGCAACGCGACCTG 994
 QY 1037 GTGAATAATGACAAACATTTCTCAAAGCTGTGATTTGCTGATTTGCTCAGTGCAGGTCAAAT 1096
 Db 995 ATAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTTCTGGAAGTGTAT 1054
 QY 1097 GGCATTGACACTCATTTTCATGAATGACAGGATGATTTCTTAATGAATTTTAAAGATCCT 1156
 Db 1055 GGGCGAGACTTACTTTTGTAGAGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1114
 QY 1157 AAAATCCAGTTGTATATGAGAGTGTACGACTTCCAGTAAACATTTTCAAAGGATCAGCC 1216
 Db 1115 AGAAATCCTGTAGTATATGGAGTCTTTACTACAAACAGCTCCATCTTCAAAGGCTCTGT 1174
 QY 1217 GTGTGATATAGCATAGTATGATGAGAGGGTGTCTTGGTCCATATGCCCCACAGG 1276
 Db 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTTAAATGGTCCATATGCTCATAG 1234
 QY 1277 GATGGACCAACTATCAATGGGTGCTTATCAAGGAAGTCCCTTATCCAGGCCAGGA 1336
 Db 1235 GAAAGTGACACATCGTTGGGTGAGTATGATGGAGAAATTTCTTATCCAGGCTGT 1294
 QY 1337 ACTGTGCCAGCAAAACATTTG- - - GTGTTTTGACTCTACAAAGGACCTTCTCTGATGAT 1393
 Db 1295 ACATGTCCAAGCAAAACCTATGACCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354
 QY 1394 GTTATAACCTTTGCAAGAGTATCCAGCCATGTAATCCAGTGTTCCTATGAACAAAT 1453
 Db 1355 GTCATCAGTTTCATAAAGGGGCACTCTGTGATGTATAAGTCCGTATATCCCAAGTTCCAGGA 1414
 QY 1454 CGCCCAATAGTATCAAAACGAGTATAATTTCAATTTACAAATTTGCTGACACGA 1513
 Db 1415 GGACCAACGTTCAAGAGATCAATGTGGTTACAGACTGACACAGATAGTGTGATCAT 1474
 QY 1514 GTGGATGCAAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT 1573
 Db 1475 GTCAATGGCAGAGATGGCCAGTACGATGTATGTTTCTTTGGAACAGACATTTGGAACCTGTC 1534
 QY 1574 CTTAAAGTAGTTTCAATTTCTTAAGGAGACTGGTATGATTTTAGAGAGGTTCTGCTGGA 1633

Db 1535 CTCAAAGTTGTGAGCAATTTCAAAGGAAAGTGG- - - AATATGGAAGAGTAGTGTCTGGAG 1591
 QY 1634 GAAATGACAGTTTTCGGGAACCGAGTCTGATTTTTCAGCAATGGAGCTTTTCCACTAAGCAG 1693
 Db 1592 GAGTTGCGAGATATTCAGGACCTCATCAATCATCTTTGAAACATGGAAATGTCTCTGAAGCAG 1651
 QY 1694 CAAACAACTATATATTTGGTTTCAAACGGCTGGGGTTGCCAGCTCCCTTTTACACGGGTGTGAT 1753
 Db 1652 CAAACAAATTTGATCATTTGGTTCCGAGATGATAGTTAGTCTCTCTTGCACAGATGCGAC 1711
 QY 1754 ATTTACGGGAAAGCGTGTGCTGAGTTTCCCTCGCCGAGACCCCTTACTGTCTTTGGGAT 1813
 Db 1712 ACTTATGGAAAGCTTGGCAGACTGTTGTCTTGGCAGAGACCCCTACTGTGTGCTGGGAT 1771
 QY 1814 GGTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAGATATA 1873
 Db 1772 GAAATGATGCTCTCGATATGCTCTTCTTAAAGGAGAGCTTAGACGCCAAGATGTA 1831
 QY 1874 AGAAATGAGACCCCACTGACTCCTGTTTCAAGACTTTACACCATGATAATCACCATGGCCAC 1933
 Db 1832 AAATATGGGACCCCAATCACCAGTGTGGGACATCGAAGACAGCATTTAGTCATG- - - AA 1888
 QY 1934 AGCCCTGAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATGCAAT 1993
 Db 1889 ACTGCTGATGAAAGGCTGATTTTGGCAATTTGAATTTTAACTCAACCTTTCTGGAATGTATA 1948
 QY 1994 CCGAAGTCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGGCGGAAATGAAGAGCGAAA 2053
 Db 1949 CCTAATCCCAACAAAGCAACTTATTAATGGTATATCCAGAGGTGAGGAGTGAAGATCGA 2008
 QY 2054 GAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGT 2113
 Db 2009 GAGGAGTTGAAGCCGATGAAGAAATCATCAACGGAATATGGCTACTGATTCGAAGT 2068
 QY 2114 CTACAAAGAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGCGGTTCATACAA 2173
 Db 2069 TTGCAGAAAGAGGATTTCTGGATGTATTACTGCAAAAGCCAGAGACACATTTTCATCCAC 2128
 QY 2174 ACTCTCTTAAAGTAAACCTCGAAGTCAATTCACAGAGCAATTTGGAGAGACTTTCTTCAT 2233
 Db 2129 ACCATGTAAGTGTGACTTTTGAATGTATTGAGATGAACAGATGGAATAATCCAGAGG 2188
 QY 2234 AAAGATGATGATG 2246
 Db 2189 GCAGAGCATGAGG 2201

RESULT 12

US-10-174-590-347
 ; Sequence 347, Application US/10174590
 ; Publication No. US20030008352A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Iuc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SMOE
 ; FILE REFERENCE: P3430R142
 ; CURRENT APPLICATION NUMBER: US/10/174,590
 ; PRIOR FILING DATE: 2002-06-18
 ; Prior application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 347
 ; LENGTH: 3871
 ; TYPE: DNA

i: ORGANISM: Homo Sapien
US-10-174-590-347

Query Match 26.5%; Score 718.6; DB 14; Length 3871;
Best Local Similarity 61.9%; Pred. No. 1.6e-202;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY	269	AATGGGAAGAACAAATGTGCCAGGCTGAATATCTCAACAGAAATGTTGGNATCCAAC	328
DB	215	ACTTTGAAGCAAAATATTCAGAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAAAT	274
QY	329	AATGTGATCACTTTCAATGCTTGGCCAGCTCCAGTATATCATACCTTCTTTTGGAT	388
DB	275	AGCTGATTTCCCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACTCTTCTCTTAGAT	334
QY	389	GAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTCATTCGACCTGGTT	448
DB	335	GAGGAAGAGGAGGCTGCTTTGGGAGCCAAAGACCAACATCTTCTACTCAGTCTGGTT	394
QY	449	AA---TATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGAA	505
DB	395	GACTTAAACAAAATTTTAAAGAGATTTATTTGGCTGCTGCAAAAGGAACGGGTGGAATTA	454
QY	506	TGCAAGTGGGCTGGAAGAGACATCTCTGAAGATGTCTAAATTTTCATCAAGTACTTTAG	565
DB	455	TGTAATTTAGCTGGGAAGATGCAATACAGAAATGTGCAAAATTTTCATCAGAGTACTTCAG	514
QY	566	GCATATAATCAGACTCACTTTGTACGCTGTGGAACGGGGCTTTTTCATCCAAATTTGCAAC	625
DB	515	CCCTATAACAAAACCTACATATATGTGTGGNACTGGAGCATTTTCATCCNATATGGGG	574
QY	626	TACATTTGAATTTGGAACATCATCTGAGGACAAATTTTTTAAGCTGGAGAACTCACATTTT	685
DB	575	TATATTTGATCTTGGAGCTTACAAGGAGGATATATATTTCAAACTAGACACACATAATTTG	634
QY	686	GAAACGGCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACACATCCCTTTTAAATA	745
DB	635	GAGTCTGGCAGAGCTGAAATGTCTTCGATCTCTCAGCAGCCTTTTCTTCAGTAATGACA	694
QY	746	GATGGAGAATTAATCTCTGGAATCTGAGCTGATTTTATGGGCGAGACTTTGCTATCTTC	805
DB	695	GATGAGTACTCTACTCTGGACAGCTTCTGATTTCTTGGCAAGATACGTGATTCAT	754
QY	806	CGAATCTTTGGGCTACTCATGACCACTACATCAGAACTGACATTTTCAGAGCACTAC	814
DB	755	CGATCCCTTTGGGCTACTCATGACCACTACATCAGAACTGACATTTTCAGAGCACTAC	814
QY	857	TGGCTCAATGATCCAAAGTTTATAGTGGCCACTCATCTCAGAGAGTCAATCTCTGAA	916
DB	815	TGGCTCAATGGAGCAAAATTTTATTTGAACTTTCTTCATACCAAGACCTTACATCCAGAT	874
QY	917	GATGACAAAGTATACCTTTTCTTCCGTGAAATGCAATAGATGAGAACTCTGGAATA	976
DB	875	GATGATAAATATATTTCTTCTTCTGATCATCTCAAGAGGCGAGTACCTCCGATAAA	934
QY	977	GCTACTCAGCTAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1036
DB	935	ACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGATGATGATGATGATGATGATG	994
QY	1037	GATGATAAATGAGCAATCTCTCAAGCTGCTGATTTGCTCAGTGGCAGGTCGAAAT	1096
DB	995	ATAAACAGTGGAGCACTTTCTTAAAGGCGAGCTGATTTGCTCAATTTCTGGAAGTAT	1054
QY	1097	GCGATTGACACTCATTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG	1156
DB	1055	GGGGCAGATACCTTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG	1114
QY	1157	AAAAATCCAGTTGATATGAGGATTTTACGACTTCCAGTAAACATTTTCAAGGATCAGCC	1216
DB	1115	AGAAATCTGTAGTATATGAGGCTTTTACTTACAAACAGCTCCATCTTCAAGGCTCTGCT	1174
QY	1217	GTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1276

RESULT 13
US-10-176-758-347

DB	1175	GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAG	1234
QY	1277	GATGAGCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGCGCAGGA	1336
DB	1235	GAAAGTGACAGACCATCGTTGGGTGAGTATGATGGAGAAATTCCTTATCCAGGCGCTGGT	1294
QY	1337	ACTTGTCCAGCAAAACATTTG---GTGGTTTGTACTCTACAAGAGACCTTCTCTGATGAT	1393
DB	1295	ACATGTCCAAGCAAAACCTTATGACCCACTGATTTAAGTCCACCGAGATTTTCCAGATGAT	1354
QY	1394	GTTTAAACCTTTTGAAGAGTCTATCCAGCATGTACAATCCAGTGTCTCTATGAACAAT	1453
DB	1355	GTATCATGTTTCATTAAGCGGCACCTCTGTGATGTATAGTCCGTATACCCAGTTGAGGA	1414
QY	1454	CGCCCAATAGTATGATCAAAACGGATGTAAATTTATCAATTTTACACAAATTTGCTGAGACGA	1513
DB	1415	GGACCAACGTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCAT	1474
QY	1514	GTGGATGCAAGAGATGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACGCTT	1573
DB	1475	GTCAATTTGCAAGAGATGGCCAGTACGATGTAAATGTTTCTTTGGAAACAGACATTTGGAACCTGTC	1534
QY	1574	CTTAAAGTATGTTTCAATTTCTTAAGGAGCTGTGATGATTTTGAAGAGGTTTCTGCTGGAA	1633
DB	1535	CTCAAGTTGTGAGCATTTTCAAGGAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG	1591
QY	1634	GAAATGACAGATTTTTCGGGAACCGACTGCTATTTTACAGCAATGGAGCTTTCCATTAAGCAG	1693
DB	1592	GAGTTGCAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGNAAGCAG	1651
QY	1694	CAACAACTATATATTGGTTTCAAGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT	1753
DB	1652	CAACAAATTTGATATTTGGTTTCCCGAGATGATTTAGTTTCACTCTCTCTTGCACAGATCGAC	1711
QY	1754	ATTTACGGAAAGCGTGTCTGAGTGTGCTCGCTCGCCGAGAGCCCTTACTGTGCTCTGGAT	1813
DB	1712	ACTTATGGGAAGCTTGGCAGACGTGTCTTCTTCCAGAGAGCCCTTACTGTGCTCTGGAT	1771
QY	1814	GCTTCTGCACTGTCTCGCTATTTTCCCACTGCAAAAGAGACGCAAGAGACAGCAAGATATA	1873
DB	1772	GGAATGCACTGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGACGCCAAGATGTA	1831
QY	1874	AGAAATGGAGCCCACTGACTCACTGTTCAGACTTACACCATGATTAATCACCATGGCCAC	1933
DB	1832	AAATATGGCAGCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTTAGTCATG---AA	1888
QY	1934	AGCCCTGGAAGAGAGATCATCTATGTTGATAGAAATAGTAGCACATTTTGTGAATGCACT	1993
DB	1889	ACTGCTGATGAAGAGTGAATTTTGGCATTTGAATTTTAACTCAACCTTTCTGGAATGATA	1948
QY	1994	CCGAAGTCCGAGAGCGCTGCTTATTTGGCAATTCAGAGCGCAAAATGAAGAGCGCAAAA	2053
DB	1949	CCTAATCCCAAGCAACTATTAAATGGTATATCCAGAGTTCAGGGATGAGCATCGA	2008
QY	2054	GAGAGATCAGAGTGGATCATATCATCATCAGACAGATCAAGGCCCTTCTGTCTACGTAGT	2113
DB	2009	GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGT	2068
QY	2114	CTACAACAGAGGATTCAGCAATTTACCTCTGCCATGCGGTGGAACATGGGTTTCATACAA	2173
DB	2069	TTGCGAAGAGAGGATTTCTGGGATGTTTACTCTCAAGCCGAGGAGCACACTTTTCATCCAC	2128
QY	2174	ACTCTTTTAAAGTAAACCTCGAAGTCTATTGACAGAGCATTTTGAAGAACTTCTTTTCAT	2233
DB	2129	ACCATAGTGAAGTCACTTTTGAATGTCATTGAGATGAACAGATGGAATATCCAGAGG	2188
QY	2234	AAAGATGATGATG 2246	
DB	2189	GCAGAGCATGAGG 2201	

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; Sequence 347, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper of Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-176-758-347

Query Match      26.5%; Score 718.6; DB 14; Length 3871;
Best Local Similarity 61.9%; Pred. No. 1.6e-202;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGAACAAATGTGCAAGGCTGAAATATCTCTACAAAGAAATGTGGAATCCAAAC 328
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QY 329 AATGTGATCACTTTCATGGCTTGGCCAAACAGCTCAGTTATCATACCTTCTTTGGAT 388
DB 275 AGCTGTATTCCTCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACTCTTCTTAGAT 334
QY 389 GAGGAACGGAGTAGGCTGTATCTGGAGCAAGAGATCATATTTTCATTCGACCTGGTT 448
DB 335 GAGGAAGAGGAGGCTGCTCTTGGAGCCAAAGACCATCTTCTACTAGCTGGTT 394
QY 449 AA---TATCAAGATTTTCAAAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAA 505
DB 395 GACTTAAACAAAATTTTAAAGATTTTATTCGCTGTGCAAGGAGGAGGCTGCAATTA 454
QY 506 TCGAAGTGGCTGGGAAGACATCTCTGAAGATCTGTAAATTTTCAATCAAGTACTTAAAG 565
DB 455 TGTAAATTAGCTGGGAAGATGCCAATACAGAAATGTGCAAAATTTTCATCAGAGTACTTCAG 514
QY 566 GCATATATATCAGACTCAGCTTGTACGCTGTGGAACGGGGCTTTTTCATCCAAATTTGCACC 625
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QY 746 GATGAGAAATATATCTCTGGAACCTCAGCTGATTTTATGGGCGGAGACTTTTGTCTATCTTC 805
DB 695 GATGAGTACCTTCTCTGGAACACTTCTGATTTTCTTGGCAAGACTTGCATCTACT 754
QY 806 CGAATCTTTGGG-----ACCAACCAACCAATCAGACAGACAGATGATTCAGG 856
DB 755 CGATCCCTTTGGGCTTACTCATGACCAACCACTACATCAGAACTGACATTCAGAGCACTAC 814
QY 857 TGGCTCAATGATCCAAAGTTTATAGTGCACCTCATCTCAGAGAGTGCAATCTCTGAA 916
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DB 815 TGGCTCAATGGAGCAAAATTTTATTGGAACTTTCTTATACACAGACACCTTACAATCCAGAT 874
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DB 875 GATGATAAATATATTTCTTCTTCGTTGAAATGCAATAGATGGAGAACACTCTTCCGATATA 934
QY 977 GCTACTCAGCTTAGAATAGGTTCAGATATGCAAGAAATGACTTTTGGAGGGCAGACAGAGTCTG 1036
DB 935 ACCATCTCTTCTCGAGTTTGGAGAGATTGTAAGAAATGATGTAGGAGGACACAGCAGCTG 994
QY 1037 GTGAATAAATGGACAAACATCTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCAAAT 1096
DB 995 ATAAACAAGTGGACGACTTTTCTTAAGCCAGACTGATTTGCTCAATTTCTTGAAGTGTAT 1054
QY 1097 GCATTGACACTCATTTTATGAACTGCAAGTGTATTTCTTAATGAACTTTTAAAGATCTT 1156
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QY 1394 GTTATAACCTTTGCAAGAGTCTATCCAGCCATGTACATCCAGTGTCTTCTATGAACAA 1453
DB 1355 GTCATCAGTTTCAATAAGCGGCACCTCTGTGATGTATAGTCCGTATATCCAGTTGCAGGA 1414
QY 1454 CGCCCAATAGTGTATCAAAACGGATGTAATTTATCAATTTTACAAATTTGCTAGACCGA 1513
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QY 1514 GTGGATGAGAAAGTGGACAGTATGATGTATTTATCGGAACAGATGTTTGGGACCGTT 1573
DB 1475 GTCATTTGCAAGATGGCCAGTACGATGATTTTCTTGGAAACAGACATTTGGAACCTGC 1534
QY 1574 CTTAAAGTATTTCAATCTTCAAGAGACTTGGTATGATTTTAGAAGAGGTCTCTGCTGAA 1633
DB 1535 CTCAAGTTGTGACATTTTCAAGGAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG 1591
QY 1634 GAAATGACAGTTTTTTCGGGAACCGACTGTATTTTCAGCAATGGAGCTTTCCACATAGCAG 1693
DB 1592 GAGTTGAGATTTTCAAGCACTCATCAATCATCTTGAACATGGAAATGTCTCTGAGAGCG 1651
QY 1694 CAACAACATATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGTAT 1753
DB 1652 CAACAATTTGATATTTGTTTCCGAGATGGAATGATTTAGTCTCAGCTCTCTCTTGCACAGATGCGAC 1711
QY 1754 ATTTACGGGAAGCGTGTGCTGAGTGTGCTCCCGAGAGCCCTTACTGTGCTTGGAT 1813
DB 1712 ACTTATGGGAAGCTTGGCAGACTGTGTGTTCTTCCAGAGACCCCTTACTGTGCTGGGAT 1771
QY 1814 GGTTCGTGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAAGACCAAGATATA 1873
DB 1772 GGAATGATGCTCTCGATATGCTCTTCTTCTTAAAGGAGAGCTAGACGCAAGATGTA 1831
QY 1874 AGAAATGGAGACCACTGACTCTGTTCTGACTTTACACCATGATATATCAACATGGCCAC 1933
DB 1832 AAATATGGCACCACCAATCAACCCAGTGTGGGACATCGAAGACAGACATTTAGTCAATG---AA 1888
QY 1934 AGCCCTCAAGAGAGATCAATCTATGTTGTAGAGATAGTAGACATATTTTGGATGAGT 1993
DB 1889 ACTGCTGATGAAAGGTGATTTTGGGCAATGATTTTAACTCAACTCTTCTGGAATGATA 1948

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RESULT 15

; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
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Query Match 26.5%; Score 718.6; DB 14; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 1.6e-202;
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QY 269 AATGGGAAGCAAAATGTCAGAGGCTGAAATATCTCTACAAAGAAATGTTGGAATCCAAC 328
 DB 215 ACTTTGAAGCAAAATATTTCCAAGACTCAAGCTAACTCAAAAGACTTGTGCTTTCAAAAT 274
 QY 329 AATGTGATCAGCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACACTTCTTTTGGAT 388
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 QY 686 GAAAACGGCCGTGGGAAGAGTCCATATGACCCCTAAAGTCTGCTGACAGCATCCCTTTTAATA 745
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 QY 746 GATGAGAAATATATCTTGGAACTGAGCTGATTTTATGGGGGAGACTTTTGTCTATCTTC 805
 DB 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAGATACTGCAATCACT 754
 QY 806 CGAACTCTTGGG-----ACCACCAACCAATTCAGGAGAGAGAGATGATTTCCAGG 856
 DB 755 CGATCCCTTGGGCTTACTCATGACCACTACATCAGAACTGACATTTTCAGAGCACTAC 814

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 10, 2005, 03:07:03 ; Search time 8640 Seconds
(without alignments)
11934.734 Million cell updates/sec

Title: US-09-774-490-1
Perfect score: 2709
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hc:*

4: gb_est3:*

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6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2052.2	75.8	2289	9	AY402637 Pan trogl
3	1764.6	65.1	2292	9	AY402638 Mus muscu
4	868.4	32.1	997	7	CN646558 ILLUMIGEN
5	723	26.7	723	4	BI870437
6	715.2	26.4	3317	3	AK052671 Mus.muscu
7	715.2	26.4	3672	3	AK028900 Mus muscu
8	712	26.3	4248	3	AK031704 Mus muscu
9	701.2	25.9	714	7	CR789306 DKE2p4590
10	674.8	24.9	679	4	BM711125 UI-E-DX1-
11	667.6	24.6	849	7	CF726328 UI-M-HBO-
12	663.8	24.5	702	4	BM723807 UI-E-EO1-
13	624.8	23.1	777	7	CF742166 UI-M-HBO-
14	622.8	23.0	763	7	CN461035 UI-M-HBO-
15	620.2	22.9	2960	3	AK043634 Mus muscu
16	620.2	22.9	3154	3	AK033597 Mus muscu
17	620.2	22.9	3292	3	AK037034 Mus muscu
18	617	22.8	3287	3	AK048364 Mus muscu
19	615.4	22.7	828	7	CN534641 UI-M-HSO-
20	609.4	22.5	832	7	CN534073 UI-M-HOO-
21	596.4	22.0	2328	9	AY407760 Homo sapi
22	594.6	21.9	729	6	CD349263 UI-M-FY0-
23	590.4	21.8	900	6	CB196368 AGENCOURT
24	588.6	21.7	889	2	BF667677 602121773

25	586.8	21.7	719	7	CK636248	UI-M-HNO-
26	581	21.4	775	5	BU703431	UI-M-FOO-
27	577	21.3	725	7	CN457302	UI-M-HNO-
28	573	21.2	754	7	CN538762	UI-M-HSO-
29	567.4	20.9	699	6	CA327319	UI-M-FY0-
30	549.8	20.3	785	7	CO428820	UI-M-HXO-
31	548.8	20.3	689	7	CN460658	UI-M-HBO-
32	548	20.2	633	7	CN295126	1700053326
33	543.8	20.1	604	4	BI183160	UNL-P-FN-
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ALIGNMENTS

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DEFINITION genomic survey sequence.
ACCESSION AY402636
VERSION AY402636.1 GI:39758619
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2319)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2319)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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ORIGIN
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Best Local Similarity 96.9%; Pred. No. 0;
Matches 2246; Conservative 0; Mismatches 70; Indels 3; Gaps 1;
QY 200 ATGGCTGGTAACTAGGATTGTCGTTCTTTCTGGGAGTATTACTTACCAAGACGA 259
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Db 1441 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1500
QY 1697 CAACTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCTTACACGGTGTGATATT 1756
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Db 1561 TAGCGGAAAGCGTGCTGAGTGTTCCTCGCCGAGAGCCCTTACTGTCTTGGGATGTT 1620
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Db 1621 TCTGCATGTTCTGCTGATTTTCCCACTGCAAGAGAGCGCACAGCGGCAAGAA 1680
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Db 1681 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1740
QY 1937 CTTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCACATTTTGGAAATGCAATCG 1996
Db 1741 CTTGAAGAGAGAAATCATCTATGTTGAGAGAAATAGTAGCACATTTTGGAAATGCAATCG 1800
QY 1997 AAGTCGACAGAGCGCTGCTGATTTGGCAATTCAGAGCGCAAAATGAAGAGCGCAAGAA 2056
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QY 2057 GAGATCAGAGTGGATGATCATATCATCAGAGAGATCAAGGCTTCTGCTAGTGTCTA 2116
Db 1861 GAGATCAGAGTGGATGATCATATCATCAGAGAGATCAAGGCTTCTGCTAGTGTAGNNNN 1920
QY 2117 CAACAGAAGGATTTCAGGCAATTAACCTCTGCCATGCGGTGGAACATGGGTTTCATACAA 2176
Db 1921 CAACAGAAGGATTTCAGGCAATTAACCTCTGCCATGCGGTGGAACATGGGTTTCATACAA 1980
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Db 1981 CTTCTTAAGGTAACCTGGAAGTCAATGACAGAGCAATTTGGAAGAACTTCTTCATAAA 2040
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QY 2477 AGGACCCAC 2485
Db 2281 AGGACCCAC 2289
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RESULT 3
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LOCUS
DEFINITION
Mus musculus SEMA3A gene, 2292 bp DNA linear GSS 15-DEC-2003
genomic survey sequence.
ACCESSION
AY402638
VERSION
AY402638.1 GI:39758621
KEYWORDS
GSS.
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SOURCE
ORGANISM
Mus musculus (house mouse)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 2292)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
2 (bases 1 to 2292)
AUTHORS
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 85.8%; Pred. No. 0;
Matches 1993; Conservative 0; Mismatches 293; Indels 36; Gaps 4;
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Db 61 AACTATGCAACCGGAAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAAAGAAATGTTG 120
QY 320 GAATCCAAATGTGATCATTTCATGGCTTGGCCAAACAGCTCCAGTTATCATCTTC 379
Db 121 GAATCCAAATGTGATCATTTCATGGCTTGGCCAAACAGCTCCAGTTATCATCTTC 180
QY 380 CTTTGTGATGAGGACCGAGTAGCTGTATCTGGAGCAAGAGATCATATATTTTCATTC 439
Db 181 CTTTGTGATGAGGACCGAGTAGCTGTATCTGGAGCAAGAGATCATATATTTTCATTC 240
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QY 500 GATGAATCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAATTTTCATCAAGTA 559
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Db 361 CTGAGGCTTATATCAGACTCAGTTGATGCTGTGGAAGTGGGCTTTTCCATCCATC 420
QY 620 TGCACCTACATGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGACTCA 679
Db 421 TGCACCTATATTTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGACTCA 480
QY 680 CATTTTGAAGCGCGCTGGGAGAGTCCATATCACCCTAGCTGCTGACAGACATCCCTT 739
Db 481 CATTTTGAAGCGCGCTGGGAGAGTCCATATCACCCTAGCTGCTGACAGACATCCCTT 540
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 DB 601 ATCTTCAGAACACTGGGACACCACTCCAAATCAGGACAGAGCAGATGATTCAGGCTG 660
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 DB 1021 TGAT 1080
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 DB 1200 ACTTTTGAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1259
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 DB 1320 GCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1350
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 QY 1697 CAACATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1756
 DB 1471 CAGCTGTACATTTGCTCAATGCGGAGTGGACAGCTTCTCTACACCGCTGTGATC 1530
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 DB 1531 TATGGCAAGCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1590
 QY 1817 TCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAAGAGCAAGATATAAGA 1876

DB 1591 TCTCATGCTCAGCTTATTTTCTTACTGCAAGAGCGCACAGAGCAAGATATAAGG 1650
 QY 1877 AATGAGAGCCCACTGACTCACTGCTTACAGACTT---ACACCATGATAATCACCATGCGCAC 1933
 DB 1651 AATGAGAGCCCACTGACTCACTGCTTACAGACTT---ACACCATGATAATCACCATGCGCAC 1710
 QY 1934 AGCCCTGAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGACATTTTGGAAATGAGT 1993
 DB 1711 AGCCTTGAAGAGAGAAATCATCTATGAGTGGAAACAGTAGTACATTTCTTGAATGAGT 1770
 QY 1994 CCGAGTCCAGAGAGCGCTGCTTATTCGCAATTTCCAGAGCGGCAATTCAGAGCGCAAA 2053
 DB 1771 CCGAGTCCAGAGAGCGCTGCTTATTCGCAATTTCCAGAGCGGCAATTCAGAGCGCAAA 1830
 QY 2054 GAAGAGATCAGAGTGGATGATCATATCATCAGAGACAGATCAAGGCTTCTGCTACGATGAT 2113
 DB 1831 GAGGAGATCAGAGTGGTGTATCATATCATCAGAGACAGACAGGCTTCTGCTCCGATGAG 1890
 QY 2114 CTACAGAGAGAGATTCAGGCAATTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2173
 DB 1891 CTGCAAGAGAGAGATTCAGGCAATTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1950
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 QY 2234 AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2293
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 QY 2294 CAGAGAGTCTGTATCAGAGATTCATGAGCTCATCAACACCCCAATCTTCAACAGATG 2353
 DB 2071 CAGAGAGTCTGTATCAGAGATTCATGAGCTCATTAACACCCCAATCTTCAACAGATG 2130
 QY 2354 GATGAGTCTGTATGAGAGTTCGGAAGGCGGCAAGAGGCGGCAAGAGGCGGCAAGAGGCGG 2413
 DB 2131 GATGAGTCTGTATGAGAGTTCGGAAGGCGGCAAGAGGCGGCAAGAGGCGGCAAGAGGCGG 2190
 QY 2414 CATACCCAGAGGAACTGATTAACAAATGGAAGCACTTCAAGAGAAATGGAAGAGTGAAGAAC 2473
 DB 2191 CACTCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2250
 QY 2474 AGGAGAGCCCAAGATTTGAGAGGCGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2515
 DB 2251 AGGAGAGCCCAAGATTTGAGAGGCGGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2292

RESULT 4

CN646558 997 bp mRNA linear EST 13-MAY-2004
 ILLUMIGEN MCQ 26534 Katze MMR Macaca mulatta cDNA clone IBIUW:8442
 5' similar to Bases 2 to 997 highly similar to human SEMA3A
 (H8.252451), mRNA sequence.

ACCESSION CN646558
 VERSION CN646558.1 GI:47160001
 LOCUS EST.
 DEFINITION Macaca mulatta (rhesus monkey)

KEYWORDS
 SOURCE Macaca mulatta
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecidae;

REFERENCE
 TITLE Large-scale Rhesus Macaque cDNA Sequencing
 AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magnus, C.L.
 JOURNAL Unpublished (2003)
 COMMENT Contact: C. Magnus
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnus@illumigen.com
 Sequenced on 2004.03.10. 794 Q20 bases.

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PCR Primers
FORWARD: CCTCTACTAAGGGAACAAA
BACKWARD: CACTATAGGGCGCAATTGGTA
Insert Length: 997   Std Error: 0.00
Plate: CL000144   row: C   column: 04
Seq primer: CCTCTACTAAGGGAACAAA
POLYA=No.

Location/Qualifiers
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   kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold
   Cloning Kit (Catalog #200450)"

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FEATURES

source

ORIGIN

Query Match	32.1%;	Score 868.4;	DB 7;	Length 997;
Best Local Similarity	94.5%;	Pred. No. 3.2e-238;		
Matches 93%;	Conservative 0;	Mismatches 46;	Indels 8;	Gaps 3;
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QY	1508	GACCGAGTGGATGCAGAAAGATGGACAGTATGATGTTATGTTATCGGAAACAGATGTTGGG	1567	
DB	62	GACCGAGTGGATGCAGAAAGATGGACAGTATGATGTTATGTTATCGGAAACAGATGTTGGG	121	
QY	1568	ACCGTCTTTAAAGTAGTTTCAATTCCTAAAGGAGACTTTGGTATGATTTAGAAAGGTTCTG	1627	
DB	122	ACCGTCTTTAAAGTAGTTTCAATTCCTAAAGGAGACTTTGGGATGATTTAGAAAGGTTCTG	181	
QY	1628	CTGGAGAAATGACAGTTTTTTTCGGGAACCGACTGCTATTTTCAGCAATGGAGCTTTCACCT	1687	
DB	182	CTGGAGAAATGACAGTTTTTTTCGGGAACCGACTACTATTTTCAGCAATGGAGCTTTCACCT	241	
QY	1688	AAGCAGCAACAACTATATATTTGGTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACGG	1747	
DB	242	AAGCAGCAACAACTATATATTTGGTTCAACAGCTGGGGTGGCCAGCTCCCTTTACACGG	301	
QY	1748	TGTGATATTTACGGGAAAGCGTGTGTGAGTGTTCCTCGCCCGAGACCTTACTGTGCT	1807	
DB	302	TGTGATATTTACGGGAAAGCGCTGTGTGTGAGTGTTCCTCGCCCGAGACCTTACTGTGCT	361	
QY	1808	TGGGATGGTCTCGATGTTCTCGGTATTTTCCCATCTGCAAGAGACGCAACAGACGCAA	1867	
DB	362	TGGGATGGTCTCTCATGCTCTCGCTATTTTCCCATCTGCAAGAGACGCAACAGACGCAA	421	
QY	1868	GATATAAGAAATCGAGACCCACTGACTCATGTTTCAGACTT---ACACCATGATAAATCAC	1924	
DB	422	GATATAAGAAATCGAGACCCACTGACTCATGTTTCGAGCTTTACACACCCAGTAATCAC	481	
QY	1925	CATGGCCACAGCCCTGAAGAGAGAATCATATCTATGTTGTAGAGAATAGTAGCAATTTTGTG	1984	
DB	482	CATGGCCACAGCCCTGAAGAGCGAAATCATCTATGTTGTAGAGAATAGTAGCAATTTTGTG	541	
QY	1985	GAATGAGTCCGAAGTCGGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGGCGAAATGAA	2044	
DB	542	GAATGAGTCCGAAGTCAACGCGAGCACTGGTCTACTTGGCAATTTCCAGAGGCGAAATGAA	601	
QY	2045	GAGCGAAAAGACAGATACAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTG	2104	
DB	602	GAGCGAAAAGACAGATACAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTG	661	
QY	2105	CTACGTAGTCTACAACAGAGAGGATTCAGGCAATTTACCTCTCGCATGCGGTGGAAACATGGG	2164	

RESULT	5
BIB70437	
LOCUS	603395690F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5405519 5'
DEFINITION	mRNA sequence.
ACCESSION	B1870437
VERSION	B1870437.1 GI:16044110
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 723) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov Plate: LILNL2034 row: c column: 24 High quality sequence stop: 723.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES

source

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ORIGIN

Query Match 26.7%; Score 723; DB 4; Length 723;
 Best Local Similarity 100.0%; Pred. No. 2.3e-196;
 Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	CAAGGATTTTCAAAGATTGTGGCCAGTATCTTTACACCAAGAAGAGATGAATCAAGTG 60
Qy	514	GGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCATCAAGGTACTTTAAGGCATATAA 573
Db	61	GGCTGGAAAGACATCTCTGAAAGAAATGTGCTAAATTTTCATCAAGGTACTTTAAGGCATATAA 120
Qy	574	TCAGACTCACTTTGACGCTGTGGAAACGGGGGCTTTTCATCCAAATTTGACCTTACATTGA 633
Db	121	TCAGACTCACTTTGACGCTGTGGAAACGGGGGCTTTTCATCCAAATTTGACCTTACATTGA 180
Qy	634	AATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCACAATTTTGAAGAACGG 693
Db	181	AATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGGAGAACTCACAATTTTGAAGAACGG 240
Qy	694	CCGTGGGAAGAGTCCATATGACCCCTAGCTCTGACAGCATCCCTTTTAAATAGATGGAGA 753
Db	241	CCGTGGGAAGAGTCCATATGACCCCTAGCTCTGACAGCATCCCTTTTAAATAGATGGAGA 300
Qy	754	ATTATATCTTGGAACTGACGCTGATTTTATGGGGGGGAGACTTTTCTCTATCTTTCCGAATCTCT 813
Db	301	ATTATATCTTGGAACTGACGCTGATTTTATGGGGGGGAGACTTTTCTCTATCTTTCCGAATCTCT 360
Qy	814	TGGGCACACCAACCCCAATCAGGACAGAGCAGCATGATTCAGGTGCGCTCAATGATCCAAA 873
Db	361	TGGGCACACCAACCCCAATCAGGACAGAGCAGCATGATTCAGGTGCGCTCAATGATCCAAA 420
Qy	874	GTTTCATTAGTGCACCACTTCATCTCAGAGAGTGACAACTCTGAAAGATGACAAAGTATATCTT 933
Db	421	GTTTCATTAGTGCACCACTTCATCTCAGAGAGTGACAACTCTGAAAGATGACAAAGTATATCTT 480
Qy	934	TTTCTTCGGTGAATAATGCAATAGATGAGAGAACACTCTTGGAAAAAGCTACTCACGCTAGAAAT 993
Db	481	TTTCTTCGGTGAATAATGCAATAGATGAGAGAACACTCTTGGAAAAAGCTACTCACGCTAGAAAT 540
Qy	994	AGGTTCAGATATGCAAGAAATGACTTTTGGAGGGGACAGAAAGTCTGGTGAATAAATGGACAAC 1053
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Qy	1054	ATTCTCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAATGGCAATTCGCACTCAATTT 1113
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Qy	1114	TGATGAATCGCAGGATGATTTCTTAAATGAACCTTTTAAAGATCCTTAAAAATCCAGTTGTATA 1173
Db	661	TGATGAATCGCAGGATGATTTCTTAAATGAACCTTTTAAAGATCCTTAAAAATCCAGTTGTATA 720
Qy	1174	TGG 1176
Db	721	TGG 723
RESULT 6		
AK052671	3317 bp	linear
LOCUS	Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630019P03 product:SEMAPHORIN 3D PRECURSOR homolog [Homo sapiens], full insert sequence.	HTC 03-APR-2004
DEFINITION		
ACCESSION	AK052671	
VERSION	AK052671.1	GI:26342870
KEYWORDS	HTC; CAP trapper.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	Carninci, P. and Hayashizaki, Y.	
TITLE	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	99279253	
PUBMED	10349636	
REFERENCE		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	

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ORIGIN

Query Match 26.4%; Score 715.2; DB 3; Length 3317;
 Best Local Similarity 62.1%; Pred. No. 6.8e-194;
 Matches 1220; Conservative 0; Mismatches 723; Indels 21; Gaps 5;

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Qy	335	ATCAGTTTCAATGGCTTGGCAACAGCTCAGTTATCATACCTTCTTTTGGATGAGGAA	394
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Qy	395	CGGAGTAGGCTGTATCTGTGAGCAAGAGTACATATTTTCATCGACCTGGTTAA--T	451
Db	782	AGGGGCTACTGCTCTAGAGCCAAAGACCATGTCTTCTGCTCAGTCTGGTGTACTTG	841
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Qy	692	GGCGTGGGAGAGTCCATATGACCTAGCTGCTGACAGCATCCCTTTTATAGATGA	751
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Qy	752	GAAATATATCTCTGGAACCTGACGTGATTTTATGGGGCGAGACTTTGCTATCTTCCGAACT	811
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Qy	812	CTTGGGC-----ACCAACCCCAATCAGACAGACAGCATGATTTCCAGGTGGCTC	862
Db	1202	CTGGGCTAATGCAGGACCACCATTCATCAGAACTGACATTCAGAGCACCCTGGCTC	1261
Qy	863	AATGATCCAAAGTTCAATAGTCCACCTCATCTCAGAGGTGCAATCTCAAGATGAC	922
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Qy	923	AAAGTATATCTTTTCTTCGCGTGAATAATGCAATAGATGGAGAACACTCTCGGAAAGCTACT	982
Db	1322	AAAATATATTTCTTCTTCGAGAAATCATCCAGGAGGAGGAGTACTTCTGACAGAGCAT	1381
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Db	1382	CTTTCAAGAGTTGGAGAGATTTGTAAAGATGATGTAGTGGGCAACAGAGTCTGTAAAC	1441
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Qy	1460	ATAGTGTATCAAAACGGATGTAATTTATCAATTTTACACAAATTTGCTAGACCGAGTGTAT	1519
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Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Riken integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
JOURNAL
MEDLINE
PUBMED 11076861

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
4		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
		Functional annotation of a full-length mouse cDNA collection		
		Nature 409, 685-690 (2001)		5

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.

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Query Match 26.3%; Score 712; DB 3; Length 4248;
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Matches 1218; Conservative 0; Mismatches 725; Indels 21; Gaps 5;

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335 ATCACTTTTCAATGCTTGGCCCAACAGCTCCAGTTATCATACCTTTCATTCGACCTGGTTAA --- T 451
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333 ATCCCCTTTTGGTTCATCAGAAGNATGGATTCGAGACTCTTTTGGATGAGAG 392
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395 CGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTTCATTCGACCTGGTTAA --- T 451
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IMAGE:30547504 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CF726328
CF726328.1 GI:37600496
EST.
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 849)
NTH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pyX-5.

FEATURES
source

Location/Qualifiers
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/note="Organ: Eye; Vector: pyX-Asc; Site: 1: EcoR I; Site: 2: Not I; The library was constructed according to Benton, Lennan and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTTATGAAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match 24.6%; Score 667.6; DB 7; Length 849;
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Matches 746; Conservative 0; Mismatches 98; Indels 2; Gaps 2;
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

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UI-E-E01-aix-o-04-0-UI.5', mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

1 (bases 1 to 702)
Normalizaton and subtraction: two approaches to facilitate gene discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road,
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).	
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ORIGIN	
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LOCUS	
DEFINITION	
ACCESSION	
VERSION	
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AUTHORS	
TITLE	
JOURNAL	
COMMENT	
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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NIH-MGC http://mgi.nci.nih.gov/	
National Institutes of Health, Mammalian Gene Collection (MGC)	
Unpublished (1999)	
Contact: Robert Strausberg, Ph.D.	
Email: cgabbs@mail.nih.gov	
Tissue procurement: Dr. James Lin University of Iowa	
cDNA library preparation: Dr. M. Bento Soares, University of Iowa	
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa	
Clone Distribution: Distribution information can be found at	
http://genome.uiowa.edu/distribution/mousefl.html	
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(BMAP)	
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ORIGIN	
Query Match 23.1%; Score 624.8; DB 7; Length 777;	
Best Local Similarity 88.7%; Pred. No. 4.8e-168;	
Matches 688; Conservative 0; Mismatches 87; Indels 1; Gaps 1;	
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RESULT 14

CN461035 763 bp mRNA linear EST 21-APR-2004
 UI-M-HB0-cpa-g-18-0-UI.r1 NIH.BMAP_HB0 Mus musculus cDNA clone
 IMAGE:30649793 5', mRNA sequence.

CN461035
 CN461035.1 GI:46466761

EST.
 Mus musculus (house mouse)

ORGANISM
 Mus musculus

REFERENCE
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 763)
 NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouseefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
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 /mol_type="mRNA"
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 /note="Organ: Eye; Vector: pYX- Asc: Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATCAAGT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
 ORIGIN

Query Match 23.0%; Score 622.8; DB 7; Length 763;
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 Matches 675; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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DB	1824	ATTGCTTTCATCGCTGCACTGCGCTAGGCGCGCCTGCGCAGATGCTGTCTGGCCCGT	1883
QY	1793	GACCTTACTGTGCTGGGATGTTTCTGCAATGTTTCTGCTATTTTCCACTGCAAAAGAGA	1852
DB	1884	GATCTTACTGCGCTGGGATGATCAGCTTTGACAGCTTCCAGCTTCCAGGCTACGGCCAAAGA	1943

Search completed: March 10, 2005, 09:35:24
Job time : 8650 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: March 8, 2005, 20:54:49 ; Search time 311 Seconds
(without alignments)
5732.363 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
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Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 2782904

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4201	85.8	771	14	US-10-262-538-10	Sequence 10, Appl
3	4201	85.8	771	14	US-10-067-632-54	Sequence 54, Appl
4	4201	85.8	771	14	US-10-247-671-164	Sequence 164, App
5	3568	72.9	655	10	US-10-320-769-3	Sequence 3, Appl
6	2245.5	45.9	777	10	US-09-946-374-310	Sequence 310, App
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8	2245.5	45.9	777	14	US-10-174-590-348	Sequence 348, App
9	2245.5	45.9	777	14	US-10-176-758-348	Sequence 348, App
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ALIGNMENTS

RESULT 1
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; Sequence 284, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KANATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

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; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-284

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Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

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US-09-774-490-1 (1-2709) x US-10-097-340-284 (1-771)

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QY 1100 ATTCACTACTATTTTGATGAATCTGAGGATGTATTCTTAATGAACTTTTAAAGATCCTAAA 1159
DB 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGATATGAGGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATACGCCGTG 1219
DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATACATGATGATGATGAGAGGCTGTTCTTGTGTCATATGCCACAGGGAT 1279
DB 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCCACTAATGGGTGCTTATCAAGGAAGAGTCCCTATCCACGCCCAAGGAACT 1339
DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCAGCAAAACATTTGGTGGTTTGTACTCTCAAAAGGACCTTCTCGATGATGTTATA 1399
DB 381 CysProSerTyrThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAAATCGCCA 1459
DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGGATGTAAATTTATCAATTTTACAAATTTGCTGAGACCGAGTGGAT 1519
DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGCAGATGATGATGTTATGTTTATCGGAACAGATGTTGGACCGTCTTTAAA 1579
DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTAGAAAGGTTCTGCTGGAAGAAATG 1639
DB 461 ValValSerIleProLysGluThrTyrAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGGCTTTTCCATTAAGCAGACAA 1699
DB 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTTGGTTCACCGGTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1759
DB 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAGCGTGTGCTGAGTGTGTGCTGCGCCGAGACCTTACTGTGCTGCTGCTGCTGCTGCT 1819
DB 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTGCTATTTTCCACTGCAAGAGAGCGCAAGACGCAAGATATTAAGAAAT 1879

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Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATAATCACCATGGCCACACGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCATGTTGTTAGAGATAGTAGACACATTTTGAATGCGAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCCACAGAGCGCTGCTGCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGACAGATCAAGCGCTTCTGCTACGTAGTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGATTCAGGCAATACCTCTGCCATCGCGTGGAAATGCTGCTACGATGCTACAA 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTACCTCGAAGTCATTGACACAGACATTTGGAAGACTTCTTCATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCACA 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGATTCATGAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCCTGTGAACAAGTTTGGAAAAGGGACCGAAACACGTCGGCAAGGGCCAGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACCTTACAGAAAAATAAGAAAGGTAGAAACAGGAG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAATTTGAGAGGGCACCCAGAGGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2

US-10-262-538-10
; Sequence 10, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-10

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)

QY 200 ATGGGCTGGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACACAAAGACA 259
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QY 260 AACTATCAGAATGGGAGAACCAATGTGCCAAGCCTGAATTTATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAAACGGAGTAGCTGTATGTTGGAGCAAAAGATCACATATTTTCATTTC 439
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTCCAAAAGATTGTGTGCCAGTATCTTACACCACAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCTCTGAAAGAAATGTCTAAATTTTCATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATTTGGACATCATCTGTAGGACATATTTTAAAGTGGAGACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAAAACGGCGCTGGGAAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAATTTACTCTCGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAACTTTGGGCACCCACCAATCAGACAGACAGACAGCATGATTTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTCAATTAGTGCACCTCATCTCAGAGAGTGACAATCTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGTACAGATATGCAAGATGACTTTGGAGGGCAGACAGATCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACAACTTCCTCAAAAGCTGCTGATTGCTCAGTGCAGGTCCAAATCGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGAACTGCGAGATGTATTCTTAATGAACCTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCAGTTGTATATGAGTGTTTAGACTTCCAGCTTAACATTTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGAGTGTGAGAGGGGTTCCTTGGTCCATATATCCACACGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360

Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319
Db 21 AsnTy rGlnAsnGlyLysAsnValProArgLeuLeuSerTy rLysGluMetLeu 40
QY 320 GAATCCAAAGTGTATCATCTTCAATGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTy rHisThrPhe 60
QY 380 CTTTTCGATCAGGAACCGAGTAGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTy rValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGATTTTCAAAAGATGTGTGCCAGTATCTTACACCAAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTy rThrArgArg 100
QY 500 GATGAATGCAAGTGGCTCGAAAGACATCCTCGAAAGATGTGCTTAATTTTCATCAAGTGA 559
Db 101 AspGluCysLeuTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCATCCAAT 619
Db 121 LeuLysAlaTy rAsnGlnThrHisLeuTy rAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTCGAAATTCGACATCATCCTCGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTy rIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTy rAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAAATTAATCTCTGAACTGCGAGCTGATTTTATGGGCGAGACTTGTCT 799
Db 181 LeuIleAspGlyGluLeuTy rSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTCTGGGCACCAACCAATCAGACAGAGCAGCATGATTCAGAGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTATAGTGCCTCCTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATCTTTTCTCCGTGAAATGCAATAGATGGAGACACTCTCGAAAGCT 979
Db 241 AspLysValTy rPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTAGATATGCAAGAAATGACTTTGGAGGGCAGCAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAATGACAAATCTCTCAAAGCTCTCTGATTTGCTCAGTGCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGAATGACAGGATGATTTCTTAATGACTTAAAGATCCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATAGAGTGTGTACGACTTCAGTAAATTTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTy rGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGTGAGAGGGTGTCTTGGTCCATATGCCCAACAGGGAT 1279
Db 341 CysMetTy rSerMetSerAspValArgValPheLeuGlyProTy rAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGGTGCCTTATCAAGGAAGATCCCTATCCAGGGCCAGGAAT 1339
Db 361 GlyProAsnTy rGlnTrpValProTy rGlnGlyArgValProTy rProArgProGlyThr 380

QY 1340 TGTCCTCCAGCAAAACATTTGGTGGTTTGTGACTCTCTACAAAGACCTTCTCTGATGATGTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGACAACTCCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTy rAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGTATCAAAACCGATGTAATATCAATTTTACAAATTTGTCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTy rGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGGACAGTATGATGTTTATTCGGAAACAGATGTTGGGACCGTCTCTAAA 1579
Db 441 AlaGluAspGlyGlnTy rAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTTAGAGAGGTCTCTCGTGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTy rAspLeuGluGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTTTCGGAAACCGACTCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTTGGTTC AACCGCTGGGTGCCAGTCCCTTTTACACCGGTGTGATTTTAC 1759
Db 501 LeuTy rIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTy r 520
QY 1760 GGGAAAGCGTGTCTGAGTGTTCCTCCCGGAGACCTTACTGTGCTTGGGATGGTCTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTy rCysAlaTrpAspGlySer 540
QY 1820 GCATGTCTCGCTATTTTCCCACTGCAAGAGACGACAGACGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTy rPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCATGACTCCTGTTTACAGCTTACACCATGATTAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAAATCATCTATGCTAGAGTAAGTAGACACATTTTGGAAATGCGAGTCCGAG 1999
Db 581 GluGluArgIleIleTy rGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGCTGCTCTATTGGCAAATTCAGAGCGCAAAATGAAGAGCGAAAGAG 2059
Db 601 SerGlnArgAlaLeuValTy rTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCGCTTCTGCTAGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATCGGTGGAAACATGCGGTTCATACAACTCT 2179
Db 641 GlnLysAspSerGlyAsnTy rLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGAAGTCAATTCACACAGAGCATTTGGAAAGAACTTCTTCAAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGAGCTCATCAACCAACCCCAATCTCAACACGATGATGAG 2359
Db 701 ValTrpTy rArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTCTGACCAAGTTTGGAAAGGACCGAAACACGTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

QY 2420 CCAGGGAACAGTAACAAATGGAGCACTTACAGAAAATAAGAAAGCTAGAAACAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAATTTGAGAGGGCACCCAGAGGTGC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4

US-10-247-671-164
 ; Sequence 164, Application US/10247671
 ; Publication No. US20030194721A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mikita, Thomas
 ; APPLICANT: Shiffman, Dev
 ; APPLICANT: Porter, Gordon, J.
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
 ; FILE REFERENCE: PA-0050 US
 ; CURRENT APPLICATION NUMBER: US/10/247,671
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: 50/323,784
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 186
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 164
 ; LENGTH: 771
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1
 US-10-247-671-164

Alignment Scores:

Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGGCTGTTAACTAGGATTCCTCTCTTTCTGGGAGTATTACTTACAGCAAGACGA 259
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 QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATATCTCAAAAGAAATGTG 319
 Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyLysGluMetLeu 40
 QY 320 GAATCCACAATGTGATCACTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyHisThrPhe 60
 QY 380 CTTTGGGATGAGCAACGGAGTAGGCTGTATGTGTGGAGCAAGCATCACATATTTTCATTC 439
 Db 61 LeuLeuAspGluLysArgSerArgLeuTyValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTAATATCAAGATTTTCAAAAGATGTGTGGCCAGTATCTTACACCAAGAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyThrArgArg 100
 QY 500 GATGAATCAAGTGGCGTGGAAACACATCTCTGAAGATGTGCTGAATTTTCATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaCysLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACCTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
 Db 121 LeuLysAlaTyAsnGlnThrHisLeuTyAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAATATTTTAAAGCTGAGAACTCA 679

Db 141 CysThrTyrlleGluileGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTGAACACGGCCGTGGGAAGAGTCCATATAGACCTTAAGCTCTGACAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGANTTATCTCTGGAACCTGAGCTGATTTTATGGGGGAGACTTTGCT 799
 Db 181 LeuileAspGlyGluLeuTySerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCCGAACCTCTTGGGCACCCACCAATCAGACAGACAGCATGATTTCCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
 QY 860 CTCATATGATCCAAAGTTCATTAGTGCCCACTCTCTCAGAGAGTGACAATCTCTCAAGAT 919
 Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuileSerGluSerAspAsnProGluAsp 240
 QY 920 GACAAAGTATATCTTTCTTCGTAAGATCAATAGATGGAGACACTCTGGAAGACT 979
 Db 241 AspLysValTyPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCAGCTAGAAATAGGTACAGATATGCAAGATGACATTTGGAGGCGACAGAACTCTGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
 QY 1040 AATAAATGGACAACATCTCTCAAGCTCTGTCTGATTTGCTCAGTGCCAGGTCCAAATGCG 1099
 Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuileCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGTAGTAACTGAGGATGATTTCTTAAGTAACTTTAAAGATCCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTTGTATATGGAGTGTTCACGACTTCCAGTAACATTTTCAAGGGATCAGCCGTG 1219
 Db 321 AsnProValValTyGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGATACATGAGTGTGAGAGGGTGTCTTGTCTCATATGCCACAGGGAT 1279
 Db 341 CysMetTySerMetSerAspValArgArgValPheLeuGlyProTyAlaHisArgAsp 360
 QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCACGCCAGGAACT 1339
 Db 361 GlyProAsnTyGlnTrpValProTyGlnGlyArgValProTyProArgProGlyThr 380
 QY 1340 TGTCCCAAGCAAAACATTTGGTGTGTTGACTCTCAAGAGGACCTTCTCTGATGATGTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValile 400
 QY 1400 ACCTTTGCAGAAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTATGAAACAATCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTGATCAAAACCGATGTAAATTTATCAATTTACAAATTTGTGTAGACCGAGTGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAAAGTGCAGATGATGTTATGTTTATCGGAACAGATGTTGGGACCGCTTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyAspValMetPheileGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTTAGAGAGGTTCTCTCGAGAGAATG 1639
 Db 461 ValValSerIleProLysGluThrTrpTyAspLeuGluValLeuLeuGluGluMet 480
 QY 1640 ACAGTTTTCGGGAACCGACTGTCTTATTTTCAGCAATGGAGCTTTTCCACTTAACAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
 QY 1700 CTATATATGTTTCAACGGCTGGGGTTCAGCTCCCTTTTACACCGGTGTGATTTTAC 1759

Db 501 LeuTyrlleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAACGCTGCTCAGTGTTCCTCGCCCGAGACCCCTTACTGTGCTTTGGAGTGTCTT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaAaGAspProTyrCysAlaIrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGACAGACGACAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCCACTGACTCAGTGTTCAGACTTACACCATGATAATCACCATGCCACACCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGAAATAGTACACATTTTTTGGAAATGCATCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGACGCTGCTTATTTGGCAATTCAGAGCGGAAATGCAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGCATCATCATATCATCAGCAGACAGATCAAGGCTTCTGCTAGTGTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTTCAGCAATTACCTCTGCCATGCGGTGGAACATGGGTTCATACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTCGTGAAGTCATGTGACAGACATTTGGAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGCTCAATAGCATGACACTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGATTCATGACGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAGTTTGGAAAGGACCGGAAACCAACACCTGCGGAAAGGCCAGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgArgGlnArgProGlyHisThr 740
QY 2420 CCAGGCAACAGTAACAATGGAAGCCTTACAGAAATTAAGAAAGTGAACACAGGAG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACCAATTTGAGAGGCGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 5

US-10-320-769-3
; Sequence 3, Application US/10320769
; Publication No. US20030158402A1
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2,
; CURRENT APPLICATION NUMBER: US/10/320, 769
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/08/556,422
; PRIOR FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-769-3
Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 14 Gaps: 0
US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)
QY 200 ATGGGCTGGTTAACTAGGATTCGTCTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGAACAAATGTGCCAAGCTGAAATTCCTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCNACAATGTCATCTTCAATGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGGATGAGCAACGGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATPATCAAGGATTTCAAAGATTTGTGTGCCAGTATCTTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGATGCAAGTGGCTGGAAAGACACATCTCTGAAAGATGCTTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCAATATAAATCAGACTCCTGTACGCTGTGGAACGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TCACCTACATTTGAATTTGACATCATCTCTGAGGACAAATATTTTAAAGCTGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAATTACTCTGGAACCTGCACTGATTTTATGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyLysLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTTGGGCACACCAATCAGACAGACAGCATCATCTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACATCTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATCTTTTCTTCCTGAAATGCAATAGATGGAGAACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyLysHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTCAGATATGCAAGAAATGACTTTTGGAGGGCACAAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATTCCTCAAGCTGCTGTGATTTGCTCAGTGCAGGTCCTCAATGGC 1099

Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACATTTTGTGATGAGTTCAGGAGTATTTCTTAATGAACTTTAAAGATCTCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelLysAspProLys 320
 QY 1160 AATCCAGTGTATATGAGTGTGTACGACTTCAGTAAACATTTTCAAGGAGTACAGCCGG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGATATATAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCAACTATCAATGGTGCCTTATCAGGAGAGTCCCTATCAGGCGCAGGAATC 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAAAACATTTGGTGGTGTGTGACTCTACAAAGGACCTTCTCATGATGTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY 1400 ACCTTTGCAAGAGTCAATCCAGCATGTACAATCCAGTGTTCCTATGAACTATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnArgPro 420
 QY 1460 ATAGTGCATCAAAACGAGTGAATATATCAATTTACACAAATTTGCTAGACCGAGTGGAT 1519
 Db 421 IleValLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAGATGGCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTATGTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCGTCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGAACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTTGTTCAACGGCTGGGTGCCAGTCCCTTTACACCGGTGTGATTTTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAGCGTGTCTGAGTGTGCTCGCCCGCAGACCTTACTGTGCTGGATGTTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGCAAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTACTGTTTACAGTTTACACCATGATTAATCACCATGGCCAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCCGAGAGCGCTGGTCTATTGGCAATTTCCAGAGCGCAAAATGAAGAGCAAAAGAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluArgLysGluGlu 620
 QY 2060 ATCAGATGGATCATATCATCAGGACAGTCAAGGCTTCTCTAGTACGTAGTCTCAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGGATTCAGCAATTTACCTCTGCGCATGGGTGGAACTGGG 2164
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

RESULT 6
 US-09-946-374-310
 ; Sequence 310, Application US/09946374
 ; Publication No. US20030073129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas P.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2830P1C1
 ; CURRENT APPLICATION NUMBER: US/09/946,374
 ; CURRENT FILING DATE: 2001-09-04
 ; PRIOR APPLICATION NUMBER: 60/098716
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098723
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098749
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098750
 ; PRIOR FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: 60/098803
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098821
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/098843
 ; PRIOR FILING DATE: 1998-09-02
 ; PRIOR APPLICATION NUMBER: 60/099536
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099596
 ; PRIOR FILING DATE: 1998-09-09
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 ; PRIOR APPLICATION NUMBER: 60/099602
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099642
 ; PRIOR FILING DATE: 1998-09-09
 ; PRIOR APPLICATION NUMBER: 60/099741
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099754
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099763
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 ; PRIOR APPLICATION NUMBER: 60/099808
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099812
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099815
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/099816
 ; PRIOR FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: 60/100385


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Db      59  IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY      395  CGAGTAGGCTGATGTTGGAGCAAAAGGATCAATATTTTCATTCGACCTGGTTAAATATC 454
Db      79  ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY      455  ---AAGGATTTTCAAAAGATTGTGCGCCAGTATCTTACACAGAGAGATGATGATCAAG 511
Db      99  AsnLysAsnPheLysLysIleTyrProAlaAlaLysGluArgValGluLeuCysLys 118
QY      512  TGGCGTGGAAAGACATCTCTGAAAGATGTGCTAAATTTTCATCAAGGTACTTAAAGGCATAT 571
Db      119  LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY      572  AATCAGACTCATTGACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATT 631
Db      139  AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY      632  GAAATTTGGACATCATCTGAGGACAATATTTTAACTGGAGAACTCACATTTGAAAC 691
Db      159  AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY      692  GCGCGTGGGAAGAGTCCATATGACCCCTAAAGCTGCTGACAGCATCCCTTTTAAATAGTGA 751
Db      179  GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY      752  GAATATATCTTGGAACTCGACTGATTTTATGGGCGAGACTTTCGTACTCTCCGAAT 811
Db      199  TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY      812  CTTGGG-----CACCAACCAATCAGACAGACGATGATTCAGGTGGCTC 862
Db      219  LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY      863  ATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGACAACTCTCAAGATGAC 922
Db      239  AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY      923  AAGATATATCTTTCTTCGTCGTAATGCAATAGATGGAGACATCTCGAAAGCTACT 982
Db      259  LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY      983  CACGCTAGTAATAGTCCAGATGATGATTTGGAGGCGACAGAGTCTGCTGAAT 1042
Db      279  LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY      1043  AATGGACAACTTCTCAAGCTGCTGATTTGCTAGTCCGAGGTCCAAATGGCAAT 1102
Db      299  LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY      1103  GACATCTATTTTGATGAATGAGGATGATTCCTTAATGAACCTTTAAAGATCCTAAAT 1162
Db      319  AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY      1163  CCAAGTTGATATGAGTGTATACGATTCAGTAACATTTTCAAGGATCAGCCGTGTGT 1222
Db      339  ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
QY      1223  ATGTATAGCATGATGATGAGAGGTGTTCTTGTGTCATATGCCACAGGGATGGA 1282
Db      359  ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY      1283  CCCAACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTATCCACGCCAGGAACTGT 1342
Db      379  AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY      1343  CCCAGCAAAACATTTGGTGGT---TTTGACTCTACAAAGGACCTTCTCGATGATGTTATA 1399
Db      399  ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418
QY      1400  ACCTTTGCAAGAAGTCAATCCAGCATGTACATCCAGTGTTCCTTATGAACATCGCCCA 1459

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Db      419  SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
QY      1460  ATAGTGATCAAAACCGATGTAAATATCAATTTTACACAAATTTGCTAGACCGAGTGGAT 1519
Db      439  ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY      1520  CGAAGAGATGACAGTATGATGATGTTATCTTCGAAACAGATGTTGGGACCGTCTTAAA 1579
Db      459  AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY      1580  GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTCTCTGCTGGAACAAATG 1639
Db      479  ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
QY      1640  ACAGTTTTCGGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCACATAAGCAGACAA 1699
Db      498  GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
QY      1700  CTATATATTTGTTCAACGCTGGGTTCGCCAGCTCCCTTTTACACCGGTGTGATATTAC 1759
Db      518  LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY      1760  GGGAAAGCGTGTGCTGAGTGTTCCTCCCGAGACCTTACTGTGCTTGGGATGGTCT 1819
Db      538  GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
QY      1820  GCATGTTCTCGTATTTTCCACTGCAAGAGAGCGCACAAAGCAGCAAGATATAGAAT 1879
Db      558  AlaCysSerArgTyrAlaProThrSerLysArgArgAlaArgGlnAspValLysTyr 577
QY      1880  GGAGACCCACTGACTCTACTGTTTCAGACTTACACCATGATATCACCATGGCCACAGCCCT 1939
Db      578  GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY      1940  GAAGAGAAATCATCTATGTTAGTAATAATAGTACACATTTTGGATGAGTCCGAG 1999
Db      597  AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY      2000  TCGCAGAGAGCGTGTCTATTGCAATTCAGAGGGGCAATGAGAGCGGAAAGAGAG 2059
Db      617  SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY      2060  ATCAGAGTGAATGATCATATCATCAGGACATCAAGAGCCCTTCTGCTAGTGTCTACA 2119
Db      637  LeuLysProAspGluArgIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY      2120  CAGAAGATTCAGCAATTTACTCTGCAATCGGTGGAAACATGGGTTCATACAACTCTT 2179
Db      657  LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY      2180  CTTAAGGTAAACCTGGGAAGTCAATGACACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
Db      677  ValLysLeuThrLeuAsnValIleGluAsnGlnMetGluAsnThrGlnArgAlaGlu 696
QY      2240  GATGATGAGATGCTCTTAAGACCAAAAGATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db      697  HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY      2300  GTCTGGTACAGAGACTTCATGCTAGCTCATCAACACCCCAATCTCAACACATGATGAG 2359
Db      711  LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY      2360  TTCTGTCAACAAGTTTCGAAAGGACCGAAACCAACGCTCGCAAGAGCCAGGACATACC 2419
Db      730  TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY      2420  CCAGGAACAGTAAACAAATGGAAGCACTTACAGAAATAATAGAAAGGTAGAAACAGGAGG 2479
Db      748  -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480  ACCCAC---GNAATTTAGAGGCGACCCAGGAGTGTCT 2512
Db      764  HisIlsArgAspLeuAspGluLeuProArgAlaVal 775

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RESULT 7
US-10-052-586-348
; Sequence 348, Application US/10052586
; Publication No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
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; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
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; PRIOR FILING DATE: 1997-12-18
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; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR APPLICATION NUMBER: 60/087208
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; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
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; PRIOR FILING DATE: 1998-06-02

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/ PRIOR APPLICATION NUMBER: 60/087827
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/ PRIOR APPLICATION NUMBER: 60/088025
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088028
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/ PRIOR APPLICATION NUMBER: 60/088033
/ PRIOR FILING DATE: 1998-06-04
/ PRIOR APPLICATION NUMBER: 60/088167
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088202
/ PRIOR FILING DATE: 1998-06-05
/ PRIOR APPLICATION NUMBER: 60/088212
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/ PRIOR APPLICATION NUMBER: 60/088217
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/ PRIOR APPLICATION NUMBER: 60/088326
/ PRIOR FILING DATE: 1998-06-04
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/ PRIOR APPLICATION NUMBER: 60/088722
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: 60/088738
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/ PRIOR APPLICATION NUMBER: 60/089653
/ PRIOR FILING DATE: 1998-06-17
/ PRIOR APPLICATION NUMBER: 60/089908
/ PRIOR APPLICATION NUMBER: 60/089908

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Alignment Scores:

Pred. No.:	2,438-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	13	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-052-586-348 (1-777)

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QY 275 AAGACAATGTCCCAAGCTGAAATATCTCAAGAAAGAAATGTGGAATCCAAACAATGTG 334
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Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuLeuSerAsnSerCys 58
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 335 ATCACTTCAATGGCTTGGCCCAACAGCTCCAGTTATCATCTTCTCTTTGGATGAGGAA 394
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Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
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QY 395 CGGAGTAGCTGTATGTGGAGCAAGGATCACATATTTTCATTCGACTGTGTTAATATC 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 455 ---AAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACGAGAGAGATGAATGCAAG 511
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 99 AsnLysAsnPhelYsIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 512 TGGGCTGGAAGACACATCTGAAAGAATGTGCTAATTTTCATCAAGGTACTTTAAGCATAT 571
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 572 AATCAGACTCACTGTAGCCCTGTGGAAGGGGGCTTTTCATCCAAATTTGCACCTACATT 631
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 632 GAAATTGGACATCATCTGAGGACAATATTTTAAAGCTGGAGAACTCACATTTTCAAAAC 691
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 692 GGCCGTGGGAAGAGTCCATATGACCTAAGCTGTGACAGCATCCCTTTTAAATAGATGA 751
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 GlyArgLeuLysCysProPheAspProGlnProPheAlaSerValMetThrAspGlu 198
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QY 752 GAATTATATCTGTGNACTGCGACTGATTTTATGGGCGAGACTTTGCTATCTTCCGAAT 811
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 812 CTGGG-----CACCAACCCCAATCAGGACAGAGCAGCATGATTCAGGTGGGCTC 862
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 863 AATGATCCAAAGTTCATTAAGTCCCACTCCTCAGAGAGTGACAAATCTCTGAAGATGAC 922
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 923 AAAGTATATCTTTCTTCCGTGAAATGCAATAGATGAGAGAACACTCTGGAAGCTACT 982
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 259 LysIleTyrPhePheArgLysSerGlnGlySerThrSerAspLysThrIle 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 983 CACGTAGATAGTGCAGATATGCAAGAAATGACATTTTGGAGGGCCACAGAACTCTGTGTAAT 1042
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
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QY 1043 AAATGGACAACATTCCTCAAAAGCTCGTCTGATTTGCTCAGTCCAGGTCCAAATGGCAAT 1102
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1103 GACACTCATTTTGTGATGACTCAGAGTGTATTCCTTAATGAATTTAAAGTCCCTAAAT 1162
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Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1163 CCAGTTGTATATGAGTGTTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTGTGT 1222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1223 ATGTATAGCATGATGATGAGAGGGTGTTCCTTGGTCCATATGCCCAAGGATGGA 1282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1283 CCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGCCCAAGGAACTTGT 1342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1343 CCCAGCAAAACATTTGGTGGT---TTTGACTCTCAAAAGGACCTTCTCTGATGATGTATA 1399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1400 ACCTTTGCAAGAAGTCAATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459
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Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTGGG-----CACCACACCAATCAGACAGACGACGATGATTCAGGTGGCTC 862
Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGlyHisTyrTrpLeu 238
QY 863 AATGATCCAAAGTTCAATAGTGCACCTCATCTCAGAGAGTGACAAATCCTCAAGATGAC 922
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAGTATATCTTTCTTCGCGTGAATGCAATAGATGGAGAACACTCTCGGAAAGCTACT 982
Db 259 LysIleTyrPhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle 278
QY 983 CAGCTAGATAGGTGAGATGCAAGATGCTTTGGAGGCGACAGAGTCTGGTGAT 1042
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGACACAACTTCCTCAAGCTCGTCTGATTGCTCAGTGCCAGGTCCAAATGGCATT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTGATGAATCAGAGATGATTCCTTAATGAATTTAAAGATCCTAAAT 1162
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CAGTTGTATATAGGTGTTTACGACTCCAGTCAACATTTTCAAGGATCAGCCGTGT 1222
Db 339 ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGATGATGATGAGAGGGTTCCTTGTGTCATATGCCACAGGATGGA 1282
Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAACTATCATGGTGCCTTATCAGGAAGAGTCCCTATCCAGGCCAGGAATGT 1342
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY 1343 CCAGCAAAACATTTGGTGGT--TTTGACTCTCAAAAGAGCTTCCTGATGATGTATA 1399
Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
QY 1400 ACCTTTGCAAGAGTATCCAGCCATGTACAAATCCAGTGTTCCTATGACCAATGCCCA 1459
Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
QY 1460 ATAGTGATCAAAACGGATGTAATTCATATTCATATTCACAAATTTGCTAGACCGAGT 1519
Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
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Db 479 ValValSerIleSerLysGluLysTrp--AsnMetGluGluValValLeuGluGluLeu 497
QY 1640 ACAGTTTTCGGGAACCGACTCTATTTCAGCAATGGAGCTTTCCTCAAGCAGCAACAA 1699
Db 498 GlnIlePheLysHisSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
QY 1700 CTATATATTGGTTCACCGCTGGGTGCTGCCAGCTCCCTTTACACCGGTGTGATTTTAC 1759
Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuLeuHisArgCysAspThrTyr 537
QY 1760 GCGAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGATGGTCT 1819
Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
QY 1820 GCATGTTCTCGTATTTTCCCACTGCAAGAGACCGCACAGACGACATATAGAAAT 1879

Db 558 AlaCysSerArgTyrAlaProThrSerLysArgArgAlaArgGlnAspValLysTyr 577
QY 1880 GGAGACCCACTCACTCACTGTTCAGACTTACACCATGATATACCATGGCCACAGCCCT 1939
Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGACAATCATATGCTGTGAGAAATAGTAGACATTTTGAATGCAGTCCGAAG 1999
Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCGCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTCTAGTAGTACAA 2119
Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAGGATTCAGGCAATTAATCTCTGCTCGGTGGAACATGGGTTTCATACAACTCTT 2179
Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY 2180 CTTAAGGTAACTCGAAAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCATAAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGAGATGGCTCTTAAGACCAAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGGTACAGAGACTTCATGACGTCAATCAACCAACCCCAATCTCAACAGATGGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGACAACTTTGAAAAGGACCGCAAAACACGTCGCAAGGCCAGGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGAAACATGAACAAATGAAGCACTTCAAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCCAAC---GAATTTGAGAGGCGCCAGGAGTGTCT 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 9
US-10-176-758-348
; Sequence 348, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430P1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-176-758-348

Alignment Scores:

Pred. No.: 2,43e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 14 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-176-758-348 (1-777)

QY 275 RAGACAAATGTCAGGCTGGAATATCTACAAAGAATGTTGGAATCCAAATGTC 334
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCATACCTTCCTTTGGATGAGAA 394
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
 QY 395 CGGAGTGGCTGTATGTTGGAGCAAGGATCATATTTTCATTCGACCTGGTTAATATC 454
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
 QY 455 ---AGGATTTCAAGATTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAG 511
 Db 99 AsnLysAsnPhelLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
 QY 512 TGGCTGGAAAGACATCTGAAAGAAATGCTGTAATTTTCATCAAGTACTTAAGGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138
 QY 572 AATCAGACTCAGTGTGACGCTGTGGACGGGGCTTTTCATCCCAATTTGCACCTACATT 631
 Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
 QY 632 GAAATTTGACATCCTCAGACAAATATTTTAACTGGAGAACTCACATTTGAAAC 691
 Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
 QY 692 GCGCTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAATAGATGA 751
 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 QY 752 GAATATATCTCTGGAATCGAGTATTTTATGGGCGAGACTTTGCTATCTTCCGAAT 811
 Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
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 Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
 QY 863 AATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGATGACAACTCTCAAGATGAC 922
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp 258
 QY 923 AAGATATATCTTTCTTCGCTGAAATGCAATAGATGGAGAACACTCTCGAAAGTACT 982
 Db 259 LysIleTyrPhePhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle 278
 QY 983 CAGCTAGAAATAGTCAGAAATGACTTTTGGAGGGCAGACAAAGTCTGGTGAAT 1042
 Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
 QY 1043 AAATGACAACTTCTCAAGCTGCTGATTGCTAGTCAGCTGCCAGGTCMAATGCATT 1102
 Db 299 LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
 QY 1103 GACACTCATTTTATGAACTGAGGATGATTCCTAATGAATCTTAAAGATCTTAAAT 1162
 Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
 QY 1163 CCAGTTGTATATGGAGTGTTCAGACTTCAGATTCAGATTCATTTTCAAGGGATCAGCCGCTGT 1222

Db 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
 QY 1223 ATGTATAGCATGATGATGAGAAGGGTGTTCCTTGGTCCATATGCCACAGAGATGCA 1282
 Db 359 ValTyrSerMetAlaAspIleAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
 QY 1283 CCCAACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTATCCAGCGCCAGAACTTGT 1342
 Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
 QY 1343 CCCACAAAACATTTGGTGGT---TTTGACTCTACAAAGGACCTCTCTCATGATGTTATA 1399
 Db 399 ProSerLysThrTyrAspProLeuLysSerThrArgAspPheProAspAspValIle 418
 QY 1400 ACCTTTTGAAGAAGTCCATCCAGCCATGATCAATCCAGTGTTCCTTATGAACATCCCCA 1459
 Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
 QY 1460 ATAGTATCAAAACCGATGTAATATCAATTTTACAAATTTGCTAGACCGAGTGGAT 1519
 Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
 QY 1520 GCAGAGATGGACATGATGTTATTCGGAACAGATGTTGGGACCGTCTTAA 1579
 Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 QY 1580 GTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTGCTGGAAGAAATG 1639
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeu 497
 QY 1640 ACAGTTTTTGGGAACCGACTGCTATTTACGCAATTTGAGAGTTCCTCAAGCAGCAACAA 1699
 Db 498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
 QY 1700 CTATATTTGTTCAACGGCTGGCTGCCAGCTCCCTTTACACGGTGTGATATTTAC 1759
 Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
 QY 1760 GGAAGAAGCTGTGCTGAGTGTTCCTCGCCCGAGAGCCCTTACTGCTTGGATGTTCT 1819
 Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaAspProTyrCysAlaTrpAspGlyAsn 557
 QY 1820 GCATTTCTCGCTATTTTCCCACTGCAAGAGACGACAGCAGCAAGATATAAGAAAT 1879
 Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577
 QY 1880 GGAGACCCACTGACTCAGTTCAGCTTACACCATGATGATAATCACCATGCCACAGCCCT 1939
 Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
 QY 1940 GAAGAGAGAATCATCTATGCTAGAGAATAGTAGACATTTTGGAAATGCAATGCCAAG 1999
 Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 QY 2000 TCCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059
 Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
 QY 2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTCTACAA 2119
 Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
 QY 2120 CAGAAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAACATGGGTTTCATACAACTCT 2179
 Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 QY 2180 CTTAAGGTAACCTCGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTCTTCATAAGAT 2239
 Db 677 ValLysLeuThrLeuAsnValIleGluAsnGlnGlnMetGluAsnThrGlnArgAlaGlu 696
 QY 2240 GATGATGGAGTGGCTCTTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAGAG 2299

Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
Qy	2300	GTCTGGTACAGAGACTTCATGCAGCTCATCAACCAACCCCAATCTCAACACCATGATGATGAG	2359
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerProAsnPhe---SerLeuAspGln	729
Qy	2360	TTCTGTGAACAAGTTTGGAAAGAGGACCGAANAACAACGTCGGCAAAAGCCAGGACATACC	2419
Db	730	TyrCysGluGlnMetTrpHisArgGluGlySarArgGlnArgAsnLysGlyGly-----	747
Qy	2420	CCAGGGAACAGCTAACAAATGGAAGCACTTACACAGAAATAAGAAAGGTAGAAAACAGGAGG	2479
Db	748	-----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg	763
Qy	2480	ACCCAC---GAATTTGAGAGGCCACCCAGGAGTGTC	2512
Db	764	HisHisArgAspLeuAspGluLeuProArgAlaVal	775

RESULT 10

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US-10-175-737-348
? Sequence 348, Application US/10175737
? Publication No. US20030013153A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Baker, Kevin P.
?
? APPLICANT: Chen, Jian
?
? APPLICANT: Desnoyers, Luc
?
? APPLICANT: Goddard, Audrey
?
? APPLICANT: Godowski, Paul J.
?
? APPLICANT: Gurney, Austin L.
?
? APPLICANT: Pan, James
?
? APPLICANT: Smith, Victoria
?
? APPLICANT: Watanabe, Colin K.
?
? APPLICANT: Wood, William I.
?
? APPLICANT: Zhang, Zemin
?
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
?
? TITLE OF INVENTION: ACIDS ENCODING THE SAME
?
? FILE REFERENCE: F3430R1C50
?
? CURRENT APPLICATION NUMBER: US/10/175,737
?
? CURRENT FILING DATE: 2002-06-19
?
? Prior Application removed - See File Wrapper or Palm
?
? NUMBER OF SEQ ID NOS: 612
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? SEQ ID NO 348
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? LENGTH: 777
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? TYPE: PRT
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? ORGANISM: Homo Sapien
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US-10-175-737-348

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Alignment Scores:

Pred. No.:	2.43e-201	Length:
Score:	2245.50	Matches:
Percent Similarity:	73.57%	Conservative:
Best Local Similarity:	54.92%	Mismatches:
Query Match:	45.86%	Indels:
DB:	14	Gaps:
		9

US-09-774-490-1 (1-2709) X US-10-175-737-348 (1-777)

Qy	275	ARAGACAATGTGCCAAGCTGAATATTATCCTCAAGAAGAAATGTTGGAAATCCACAAATGTG	334
Db	39	LysGlnAsnIleProArgLeuLysLeuThrTyrIysAspLeuLeuSerAsnSerCys	58
Qy	335	ATCACCTTTCAAATGGCTTGCCCAACAGCTCCAGTTATCATACATTCCTCTTTGGATGAGGAA	394
Db	59	IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu	78
Qy	395	CGGAGTAGGCTGTATGTTGGACAAAGGATCACATAATTTTCATTCGCCTGGTTTAATATC	454
Db	79	ArgGlyArgLeuLeuGlyAlaLysAspHisilePheLeuSerLeuValAspLeu	98
Qy	455	---AAGGATTTCAAAGATTGTGGCCAGTAGTACTTACCAGAACAGATGAATCGAAG	511
Db	99	AsnLysAsnPheLysLysilefrrPrroAlaalalysLysGluArgValGluLeuCysLys	118

QY	512	TGGGCTGGAAAAGACATCTCTGAAAGAAATGTGCTAATTTCATCAAGGTACTTAAAGGCATAT	571
Db	119	LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIeArgValLeuGlnProTyr	138
QY	572	AATCAGACTCATCTGTAGCCCTGTGGAAACGGGGCTTTTCATCAAATTTGCACCTACATT	631
Db	139	AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle	158
QY	632	GAATTTGGACATCATCTCGAGGACAAATATTTTAAAGCTGGAGAACTCACATTTTGGAAAAC	691
Db	159	AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer	178
QY	692	GGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATCGA	751
Db	179	GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu	198
QY	752	GAATATATCTCTGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCTATCTTCCGAAC	811
Db	199	TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer	218
QY	812	CTTGGG-----CACCCACCCCAATCAGGACAGCAGCATGATCCAGGTGCCTC	862
Db	219	LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu	238
QY	863	AATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGCATCTGAGAGATGCAC	922
Db	239	AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp	258
QY	923	AAAGTATACTTTTCTTCCTCGTGAATAATGCAATAGATGGAGAACACTCTGGAAGACTACT	982
Db	259	LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle	278
QY	983	CACGCTAGATAGTTCAGATATGCAAGAATGACTTTTCGAGGGCACAGAACTGTGGTGAAT	1042
Db	279	LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn	298
QY	1043	AAATGGACAACATTCCTCAAAAGTCGTCTGATTTGCTCAGTGCAGGTCCAAATGGCAT	1102
Db	299	LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla	318
QY	1103	GACACTCATTTTGATGAACCTGCAGGATGTATCTCTAATGAACCTTAAAGATCCTTAAAT	1162
Db	319	AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn	338
QY	1163	CCAGTTGTATATGAGGTGTTTACGACTTCAGATTAACATTTTCAAGGATCAGCGCTGTGT	1222
Db	339	ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys	358
QY	1223	ATGTATAGCATGATGTGTGAGAAGGGTGTCTCTGGTCCATATGCCACAGGATCGGA	1282
Db	359	ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer	378
QY	1283	CCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGAAC	1342
Db	379	AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys	398
QY	1343	CCAGCAAAAACATTTGGTGTGTTTGTGCTCTACAAAGGACCTTCTCTGATGATGTTATA	1399
Db	399	ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
QY	1400	ACCTTTTGCAGAAGATCATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGCCCA	1459
Db	419	SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro	438
QY	1460	ATAGTGATCAAAACGGATGTAATATCAATTTACAAATTTGCTGTAGACCGAGTGGAT	1519
Db	439	ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle	458
QY	1520	GCAGAAGATCGACATGATGTTATGTTTATCGGACACAGATCTGTGGACCGTCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGATGATTTAGAACAGGTTCTGCTGGAGAAGATG	1639


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Db 479 ValValSerIleSerLysGluValYsrp---AsnMetGluGluValValValLeuGluGluLeu 497
QY 1640 ACAGTTCCTGCGAAGCGGCTGCTATTTCCAGCAATGGAGCTTTCCACTTAAGCAGCAACAA 1699
Db 498 GlnIlePheLysHisSerIlelleleuAsnMetGluLeuSerLeuLysGlnGln 517
QY 1700 CTATATATTGTTCAACCGCTGGGTGCGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY 1760 GGGAAAGCGTGTCTGAGTTCCTCGCCGAGACCTTACTGTCTGGATGGTCT 1819
Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgPheProTyrCysAlaTrpAspGlyAsn 557
QY 1820 GCATGTTCTCGCTATTTCCCACTGCAAGAGCGCACAAAGACGACCAAGATATAAGAAAT 1879
Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577
QY 1880 GGAGACCCACTGACTACTGTTTCAGACTTACACCATGATTAATCACCAGCCAGCCCT 1939
Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGAGATCATCTATGCTGATAGATAGTACACATTTTGGAAATGCAGTCCGAG 1999
Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCGCAGAGAGCGCTGCTATTGGCAATTCAGAGCGGCAAAATGAAGCGGAAAGAGAG 2059
Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspLysHisArgGluGlu 636
QY 2060 ATCAGAGTGGATGATCATATCATCATCAGGACAGATCAAGGCTTCTGCTAGTACTACAA 2119
Db 637 LeuLysProAspGluArgIlelleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAGGATTTCAGGCAATTACTCTGCGCATGGGTGGAACTGGTTCATCAAACTCTT 2179
Db 657 LysLysAspSerGlyMetTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY 2180 CTTAAGTAAACCTGGAAGTCAATGCACAGACAGATTTTGGAAAGAACTTCTCATAAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGGAGATGGCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGTGACAGACTTCATGCTCATCAACCCCACTCAACACGATGGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGCAAAACAGTCGCAAGGCCAGGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGGAACAGTAACAATAGGAGCATTCAAGAAATATAAGAAAGGTAGAAACAGGAGG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCAC---GAATTGAGAGGCGCCAGGATGTC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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RESULT 11

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US-10-174-581-348
; Sequence 348, Application US/10174581
; Publication NO. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
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; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
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; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
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; PRIOR APPLICATION NUMBER: 60/080107
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; PRIOR APPLICATION NUMBER: 60/080194
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; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
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 ; PRIOR APPLICATION NUMBER: 60/081049
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 ; PRIOR FILING DATE: 1998-06-12
 ; PRIOR APPLICATION NUMBER: 60/089105
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 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653

Alignment Scores:

Pred. No.:	2.43e-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	14	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-174-581-348 (1-777)

Qy	275	RAGAACATGTGCCAAGCTGAATATCTTACAAAGAAATGTTGGAATCCAAATGTG	334
Db	39	LysGlnAsnIleProArgLeuLysLeuThrLysAspLeuLeuLeuLeuLeuSerAsnSerCys	58
Qy	335	ATCATTTCATATGCTTGGCCACACAGCTCCAGTTATCATCTTCCTTTTGGATGAGGAA	394
Db	59	IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu	78
Qy	395	CGGAGTAGGCTGTATGTTGGACAAAGATCACATATTTTCATTCGACCTGGTTAATATC	454
Db	79	ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuLeuValAspLeu	98
Qy	455	---AAGGATTTTCAAAGATTGTGCGCCAGTATCTTACACAGAGAGATGAATGCAAG	511
Db	99	AsnLysAsnPheLysLysIleTyrTrpProAlaLysGluArgValGluLeuLysLys	118

512 TGGCGTGGAAAGACATCTCTGAAAGAAATGCTGTAATTTTCATCAAGGTACTTAAGGCATAT 571
 Db ValValSerIleSerLysGluLysTrp---AenMetGluGluValValLeuGluGluLeu 497
 119 LeuAlaGlyLysAspAlaAenThrGluCysAlaAenPheIleAargValLeuGlnProTyr 138
 572 AATCAGACTCATTGTACGCTGTGAAACGGGGCTTTTCATCCAAATTTGCACCTACATT 631
 Db AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
 632 GAAATTTGGACATCCTCAGGACCAATATTTTAAAGCTGGAGCACTCACATTTTGAAC 691
 Db AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAenLeuGluSer 178
 692 GCGCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGCACAGCATCCCTTTAATAGATGA 751
 Db GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 752 GAATATATCTCTGGAAGTGCAGCTGATTTTATGGGCGGAGACTTTCCTATCTTCCGAAGCT 811
 Db TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
 812 CTTGGG-----CACCACCAACCAATCAGGACAGCAGCATGATTCAGGTGGCTC 862
 Db LeuGlyProThrHisAspHisIleTyrIleAargThrAspIleSerGluHisTyrTrpLeu 238
 863 AATGATCCAAAGTTGATAGTCCACCTCATCTCAGAGAGTGACAACTCCTGAAGATGAC 922
 Db AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
 923 AAGATATCTCTTCTCGTGAAGTGAATGCAATAGATGGAGAACACTCTCGGAAGCTACT 982
 Db LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
 983 CACGCTAGTAATAGTGCAGATGCAAGAAATGACTTTGGAGGGCAGACAGTCTGGTGAAT 1042
 Db LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAen 298
 1043 AATGAGAACATCTCCTCAAGCTGCTGATTTGCTCAGTCCAGGTCCAAATGGCATT 1102
 Db LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
 1103 GACACTCATTTCAGTCACTCAGGATGATTCCTTAATGAACTTTAAAGATCCTAAAT 1162
 Db AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAen 338
 1163 CAGATTGTATGAGGTGTTTACGACTTCAGTAACATTTTCAAGGGATCAGCGGTGTGT 1222
 Db ProValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
 1223 ATGTATAGCATGATGTGAAGGGTTCCTTGGTCCATATGCCACAGGATGA 1282
 Db ValTyrSerMetAlaAspIleAargAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
 1283 CCNACTATCAATGGGTGCTTATCAAGAGAGTCCCTATCCAGCGGACGAACTTGT 1342
 Db AlaAspHisArgTrpValGlnTyrAspGlyArgGileProTyrProArgProGlyThrCys 398
 1343 CCAGCAAAACATTTTCGTGT---TTTGACTTCACAAAGGACCTTCTCATGATGTTATA 1399
 Db ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
 1400 ACTTTTGCAGAAAGTCCATCCAGCCATGTACATCCAGTGTTCCTATGAAACATCCGCCA 1459
 Db SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
 1460 ATAGTATCAAAACGATGTAATTTATCAATTTACACAAATTCCTGCTAGACCGGTGAT 1519
 Db ThrPheLysArgIleAenValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
 1520 GCAGAGATGGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGTCTTAA 1579
 Db AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 1580 GTAGTTTCAATTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTCTCTGCTGGAAGAAATG 1639

479 ValValSerIleSerLysGluLysTrp---AenMetGluGluValValLeuGluGluLeu 497
 1640 ACAGTTTTCGGGAACCGACTCTATTTCAGCAATGGAGCTTTTCACCTAAGCAGCAACAA 1699
 Db GlnIlePheLysHisSerSerIleIleLeuAenMetGluLeuSerLeuLysGlnGln 517
 1700 CTATATATTTGGTTCAACGGCTGGGTGCCAGTCCCTTTTACCGGGTGTGATTTATAC 1759
 Db LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
 1760 GGGAAAGCGTGTGCTGAGTGTGCTGCCCGCAGACCTTACTGTCTGGATGGTCTCT 1819
 Db GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAen 557
 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCCACAAAGACGACCAAGATATAGAAAT 1879
 Db AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577
 1880 GGAGACCACTGACTCCTGTTTCAGTTCACCATGATATACCATGGCCACACGCCCT 1939
 Db GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
 1940 GAAGAGAGATCATCTATGTTGTAGATACTAGCACATTTTTCGAATGCAGTCCGAAG 1999
 Db AspGluLysValIlePheGlyIleGluPheAenSerThrPheLeuGluCysIleProLys 616
 2000 TCGCAGAGACCGCTGCTCTATTGGCAATTCACAGCGCGCAATTCAGAGAGCAAGAGAG 2059
 Db SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
 2060 ATCAGAGTGGATGATCATATCATAGACAGATCAAGGCTTCTGCTAGTGTATACAA 2119
 Db LeuLysProAspGluArgIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
 2120 CAGAGAGTTCAGGCAATTCCTCTGCCATCGGTGGACATGGTTCATACAACTCTT 2179
 Db LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 2180 CTTAAGGTAAACCTCGAAGTCAATTCACACAGACGATTTTGGAAAGAACTTCTTATAAAGAT 2239
 Db ValLysLeuThrLeuAsnValIleGluAenGluGlnMetGluAenThrGlnArgAlaGlu 696
 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCCAAG 2299
 Db HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 2300 GTCTGGTACAGAGACTTCATGCGACTCATCAACACCCCAATCTCAACAGATGATGAG 2359
 Db LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 2360 TTCTGTGAACAGTGTGGAAAGGGACCGCAAAACAACTGCGCAAGGCCAGCATACC 2419
 Db TyrCysGluGlnMetTrpHisArgGluLysArgArgGlnArgAsnLysGlyGly----- 747
 2420 CCAGGAAACAGTAACAAATGGAGCACTTACAAGAAAAATAAGAAAGTTAGAACAGAGG 2479
 Db -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAenArgArg 763
 2480 ACCAC---GAATTTGAGGAGGCCACCCAGGAGTGTCT 2512
 Db HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 12

; US-10-176-483-348
 ; Sequence 348, Application US/10176483
 ; Publication No. US20030017541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.

```

; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-176-483-348

Alignment Scores:
Pred. No.: 2,43e-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 14 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-176-483-348 (1-777)

QY 275 AAGAACAAATGTCAGGCTGAAATATCTCAAGAAAGATGTTGGAAATCCAAACATGTG 334
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 335 ATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCACTCTCTTTTGGATGAGGA 394
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 395 CGAGTAGGCTGTATGTCGAGCAAGATCATATTTTCAATCGACCTGGTTAATATC 454
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 455 ---AGGATTTTCAAGATTTGTCGAGCAAGATGTCGAGTATCTTACAGAGAGATGAGTGAAG 511
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 99 AsnLysAsnPheLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 512 TGGGCTGGAAAGACATCTGAAAGAAATGCTGCTAAATTTTCATCAAGTACTTAAGGCATAT 571
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 572 AATCAGACTCATTTGACGCTGTGGAACGGGGCTTTTCATCCAATTTGCACCTACATT 631
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 632 GAAATTTGGACATCATCTGAGACAAATATTTTAACTGGAGAACTCACATTTTGAAGAAC 691
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuLeuSer 178
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 692 GCGCTGGGAAGAGTCCATATGACCTAAGCTGCTGACAGCATCTCTTTTAAATAGATGA 751
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 752 GAATTTACTCTGGAACCTGACTGATTTTATGGGCGAGACTTTGCTTATCTTCCGAAT 811
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 812 CTTGGG-----CACCAACCACTCCAGACAGACGACGATGATCCAGGTGGCTC 862
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 863 AATGATCCAAAGTTCAATAGTCCCACTCTCATCTCAGAGAGTGAACAATCTCGAAGATCAC 922
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258

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QY 923 AAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAGAGTACT 982
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 259 LysIleTyrPhePhePheArgGluSerGlnGluGlySerThrSerAspLysThrIle 278
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 983 CACGCTAGATAGTTCAGATATGCAAGATGATCTTTGGAGGCAACAGAGTCTGTGTAAT 1042
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1043 AAATGGCAACATCTCCTCAAGCTCGTCTGATTTCTCAGTCCAGGTCCTCAATGGCAT 1102
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1103 GACACTCATTTTGAATGAACTGAGGATGATTTCTTAAATGAATTTAAAGATCCTAAAAAT 1162
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1163 CCAGTTGTATATGGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGGATACGCGCTGTGT 1222
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1223 ATGTATAGCATGAGTGTGAGAGGCTTCTTCTTGTCTCATATGCCACAGGATGGA 1282
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1283 CCCAACTATCAATGGTGCCTTTATCAAGGAAGAGTCCCTATCCACGGCCAGGAACTTGT 1342
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 379 AlaAspHisArgTyrValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1343 CCCAGCAAAACATTTTGGTGGT---TTTGACTCTCAAAAGGACCTTCTCTGATGATGTTATA 1399
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1400 ACCTTTGCAAGAAGTCCATCCAGCCTATCAATCCAGTGTCTTCTATCAACAATCGCCCA 1459
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyPro 438
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTTACAAAATTTGCTGAGACCGAGTGGAT 1519
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1520 GCAGAGATGACAGATGATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTTAAA 1579
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1580 GTAGTTTCAATTTCTAAGGACTTGGTATGATTTAGAGAGAGTCTCTCTGGAAGAAATG 1639
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGlu 497
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1640 ACAGTTTTCGGGAACCGACTGTATTTTCAGCAATGGAGCTTTCCACTTAAGCAGCAACA 1699
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 498 GlnIlePheLysHisSerSerIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln 517
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1700 CTATATATGTTTCAACGGCTGGGTGCCAGCTCCCTTTACACCGGTGATATTTAC 1759
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1760 GGGAAAGCTGTGCTGAGTGTGCTCGCCCGACACCTTACTGCTTGGATGGTGTCT 1819
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1820 GCATGTTCTCGCTATTTTCCACGTGCAAGAGACGCAAGACGCAAGATATAGAAT 1879
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr 577
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1880 GGAGACCCACTGACTCTGTTTCAGACTTACACCATGATATACCATGGCCACAGCCCT 1939
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1940 GAAGAGAGATCATCTATGTTGTAGAAATAGTAGACATTTTTCGATGAGTCCCGAAG 1999
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2000 TCGCAGAGAGCGCTGTGCTCTATTGGCAATTTCAGAGGCGAATTAAGACGCAAGAGAG 2059

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Db 617 SerGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
QY 2060 ATCAGAGTGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAGTCTACAA 2119
Db 637 LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
QY 2120 CAGAGGATTCAGGCAATACCTCTGCCATGCGGTGGGAACATGGGTTCATAAACTCTT 2179
Db 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
QY 2180 CTTAAGTAACTCGAAGCTGATGACACAGAGCATTTGGAAGAACTTCTTCATAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAenGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCATAGATGACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGTAGACAGACTTCATGAGCTCATCAACCCCACTCAACAGATGATGAG 2359
Db 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTGGAAGAGGACCGCAACACACGTCCGCAAGGCCAGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGACACAGTAACAAATGGAAGACACTTACAGAAATAAGCAAGGTAGAAACAGGAGG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCAC--GAATTTGAGAGGACCCAGGAGTGTC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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RESULT 13

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US-10-176-749-348
; Sequence 348, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-348

```

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Alignment Scores:
Pred. No.: 2,436-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 14 Gaps: 9

```

US-09-774-490-1 (1-2709) x US-10-176-749-348 (1-777)

```

QY 275 AAGAACAAATGTGCGAAGGCTGAAATATTCCTACAAAGAAATGTTGGAATCCCAACATGTG 334
Db 39 LysGlnAenIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTGCGCCAAACAGCTCCAGTTATCATACCTCTCTTTTGGATGAGGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY 395 CGAGTAGGCTGTATGTTGGAGCAAGGATCATATTTTCATTTCCGACTGGTGAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGGATTTTCAAAAGATTGTGGCCAGATATCTTACACAGAGAGATGAATGCAAG 511
Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuCysLys 118
QY 512 TGGCGTGGAAAGACATCCTGAAGAATGTGCTAAATTTTCATCAAGTACTTAAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY 572 AATCAGACTCACTTGTAGCCCTGTGGAAGCGGGGCTTTTCATCCAATTTGCACTACAT 631
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATTTGGACATCTCTGAGACAAATATTTTAAAGCTGGAGAACTCACATTTTGAAC 691
Db 159 AspLeuGlyValTyrLysGluAspIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GCGCTGGAGAGTCCATATGACCCCTAAGCTGTGACAGACATCCCTTTTAATAGATGGA 751
Db 179 GlyArgLeuLysCysPheProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAAATATATCTCTGGAACCTGCAGCTGATTTATGGGCGAGACTTTGCTATCTTCCAACT 811
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTGGG-----CACACACCAATCAGACAGACAGCATGATTTCCAGGTGGCTC 862
Db 219 LeuGlyProThrHisAspHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 ATGATCCAAAGTTTCATTAGTCCACCTCATCTCAGAGAGTGAACATCTCCTCAAGATGAC 922
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAAATATATCTTTTCTCCGTGAAAATGCAATAGATGGAGAACACTCTCGAAAAGCTACT 982
Db 259 LysIleTyrPhePhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY 983 CACGCTAGAATAGTGCAGATATGCAAGATGATTTGGAGGCGCACAGAACTCTGGTGAAT 1042
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACTTCTCAAGCTCGTCTGATTTGCTAGTCCAGTCCAGGTCCAATGGCATT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCAATTTGATGAACCTGCAGATGTATTCTTAATGAACCTTTAAAGATCCTAAAT 1162
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CCAGTTGTATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGATCAGCCGCTGT 1222
Db 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGATGTGAGAGGCTTCTTCTTGTCTCATATGCCACAGGGATGGA 1282
Db 359 ValTyrSerMetAlaAspIleAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTATCCAGGGCAGGAACCTGT 1342
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398

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1343	QY	CCAGCAAAACAATTGGTGGT---TTTGACTCTCAAAAGGACCTTCTGTAGTGTATA	1399
399	Db	ProSerLysThrTyArgAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
1400	QY	ACCTTTGCCAAGAAGTCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCGGCCA	1459
419	Db	SerPheIleLysArgHisSerValMetTyLysSerValTyProValAlaGlyGlyPro	438
1460	QY	ATAGTGATCAAAACCGGATGTAATTAATCAATTTACACAAATGTCGTAGACCGAGTGGAT	1519
439	Db	ThrPheLysArgIleAsnValAspTyArgLeuThrGlnIleValValAspHisValIle	458
1520	QY	GCAGAAGATCGACAGTAGTATGTTATCTTTATCGAACACATGTTGGACCGTCTTAAA	1579
459	Db	AlaGluAspGlyGlnTyArgValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
1580	QY	GTAGTTTCAATTCCTAAGGAGACTGTGTATGATTAGAACAGGTTCTGCTGGAAGAAATG	1639
479	Db	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluLeu	497
1640	QY	ACAGTTTTTCGGNACCGACTGCTATTTCAGCAATGGAGCTTTCCTACTAAGCAGCAACAA	1699
498	Db	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGln	517
1700	QY	CTATATATTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGATATTAC	1759
518	Db	LeuTyIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTy	537
1760	QY	GGGAAACGGTGTGCTAGTGTTCCTCGCCGAGACCTTACTGTGCTCGGATGGTTCT	1819
538	Db	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyCysAlaTrpAspGlyAsn	557
1820	QY	GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCACAGACGACGAAGATATAAGAAAT	1879
558	Db	AlaCysSerArgTyAlaProThrSerLysArgAlaArgGlnAspValLysTy	577
1880	QY	GGAGACCCTACTACTGTTCCAGACTTACCCATGATATCACCATGCCACAGCCCT	1939
578	Db	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
1940	QY	GAGAGAGATCATCATGCTGTAGAGAAAGTAGTAGACATTTTGGNATGCATCCGAG	1999
597	Db	AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
2000	QY	TCGCAGAGCGCTGTGTTATTCGCAATTCAGAGCGCAATCAAGACGCAAAAGAGAG	2059
617	Db	SerGlnGlnAlaThrIleLysTrpTyIleGlnArgSerGlyAspGluHisArgGluGlu	636
2060	QY	ATCAGATGATGATCATATCATCATCAGACAGATCAAGCCCTTCTGTACTGTACTACAA	2119
637	Db	LeuLysProAspGluArgIleIleLysThrGluTyGlyLeuLeuIleArgSerLeuGln	656
2120	QY	CAGAAGATTTCAGCAATTACCTCTGCATCGCGTGGAAACATGGTTTCATACAACTCTT	2179
657	Db	LysLysAspSerGlyMetTyTyCysLysLeuAlaGlnGluHisThrPheIleHisThrIle	676
2180	QY	CTTAAGTAAACCTGGAGTTCATGTACACAGACATTTTGGAGAACTTCTTCAATAAGAT	2239
677	Db	ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu	696
2240	QY	GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCTCAATAGCATGACACCTACCCAGA	2299
697	Db	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
2300	QY	GTCTGGTACAGAGACTTCATCGAGCTCATCAACCCACCCCAATCTCAACCATGGATG	2359
711	Db	LeuArgTyLysAspTyIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729
2360	QY	TTCTGTGACAAAGTTTGGAAAAGGACCGGAAACACAGCTCGGCAAGGCCAGACATACC	2419
730	Db	TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly-----	747
2420	QY	CCAGGNAACAGTACAAATGGAAGCACTTACAGAAAAATAAGAAAGTAGTAACAGGAGG	2479

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Db      748 -----ProLysTriPlyHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY      2480 ACCCAC---GAATTTGAGAGGGCCACCCAGGAGTGTC 2512
Db      764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 14
US-10-176-914-348
; Sequence 348, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430PLC83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-348

Alignment Scores:
Pred. No.:      2,43e-201      Length:      .777
Score:          2245.50      Matches:      413
Percent Similarity: 73.67%      Conservative: 141
Best Local Similarity: 54.92%      Mismatches: 177
Query Match:      45.86%      Indels:      21
DB:              14      Gaps:      9

US-09-774-490-1 (1-2709) x US-10-176-914-348 (1-777)

QY      275 AAGACAAATGTGCCAAGCTGAATTCCTACAAAGAAATGTTGGAATCCAAACAATGTG 334
Db      39  LysGlnAsnIleProArgLeuLysLeuThrTyrlsAspLeuLeuLeuSerAsnSerCys 58
QY      335 ATCACTTTCAATGGCTTGGGCGACAGCTCCAGTTCATCATCTCTCTTTGGATCAGGAA 394
Db      59  IleProHeuLeuGlySerSerGluGlyLeuAspHeGlnThrLeuLeuLeuAspGlu 78
QY      395 CGGAGTAGCTGTATGTGGAGCAAGATCACATATTTTCATTCGACTGGTTAAATC 454
Db      79  ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIleHeLeuLeuSerLeuValAspLeu 98
QY      455 ---AAGATTTTCAAAAGATGTGTGGCCAGTACTTTACACCAAGAGAGATGAATGCAAG 511
Db      99  AsnLysAsnPheLysLysIleTyrlProAlaLysGluArgValGluLeuCysLys 118
QY      512 TGGGCTGGAAAAAGACATCCTTGAAAGAATGTGCTTAATTCATCAAGGTACTTAAAGGCATAT 571
Db      119  LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY      572 AATCAGACTCATCTGTAGCTGTGGAGCGGGGCTTTTCATCCAAATTTGCACCTACATT 631
Db      139  AsnLysThrHisIleTyrlValCysGlyThrGlyAlaPheHisProIleCysGlyTyrlle 158
QY      632 GAAATTGGACATCATCTCGAGGACAAATATTTTAAAGCTGGGAAACTCATATTTTGAAC 691
Db      159  AspLeuGlyValTyrlLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGlySer 178

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Qy	692	GGCGTGGGAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGGA	751
Db	179	GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu	198
Qy	752	GAATTATCTCGAACTGCAGCTGATTTTATGGGCGAGACTTGTCTATCTCCGNACT	811
Db	199	TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer	218
Qy	812	CTTGGG-----CACCAACCCCAATCAGGACAGCAGCATGATTCACAGTGGCTC	862
Db	219	LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu	238
Qy	863	AATGATCCAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAACTCTGAAGATGAC	922
Db	239	AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAspAsp	258
Qy	923	AAAGTATATCTTTCTTCCTCGTGAATAATGCAATAGATGGAGAACACTCTGGAAAGCTACT	982
Db	259	LysIleTyrPhePhePheArgGluSerSerGlnGlySerThrSerAspLysThrIle	278
Qy	983	CACCTAGAATAGTTCAGATATGCAAGAAATGACATTTGGAGGGCACAAAGTCGTGAAT	1042
Db	279	LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn	298
Qy	1043	AAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGGCAGGTCCTCAAAATGGCATT	1102
Db	299	LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla	318
Qy	1103	GACACTCATTTTGATGAACTGCAGGATGATTCCTAATGAACCTTTAAAGATCCTAAAT	1162
Db	319	AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn	338
Qy	1163	CCAGTCTATATGAGAGTTTACGACTTCAGATTAACATTTTCAAGGATCAGCGCTGTG	1222
Db	339	ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys	358
Qy	1223	ATGTATAGCATGATGTGAGAAAGGGTGTCTCGTCCATATGCCACAGGATGGA	1282
Db	359	ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer	378
Qy	1283	CCCACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGACTGTG	1342
Db	379	AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys	398
Qy	1343	CCAGCAAAACATTTGGTGT---TTTGACTCTACAAGAGACCTTCCTCGATGATGTATA	1399
Db	399	ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
Qy	1400	ACCTTTTCCAAGAGTCTATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA	1459
Db	419	SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro	438
Qy	1460	ATAGTGATCAAAACCGAGTAAATATCAATTTACAAATGTGCTGACCGAGTGGAT	1519
Db	439	ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle	458
Qy	1520	GCAGAAATGCACAGTATGATTGTTATCTTTATCGGAACAGATGTTGGACCGTCTTAAA	1579
Db	459	AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
Qy	1580	GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTATAGAAGAGGTTCCTGCGAAGAATG	1639
Db	479	ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu	497
Qy	1640	ACAGTTTTTCGGGAACCGACTGCTATTTCAGCAATGGAGCTTTCCACTAAGCAGCAACAA	1699
Db	498	GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGlnGln	517
Qy	1700	CTATATATTTGGTTCACAGCGCTGGGTGGCCAGCTCCCTTTTACACCGGTGTGATATTAC	1759
Db	518	LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537

Qy	1760	GGGAAACGGTGTGCTGAGTGTTCCTCGCCGCGAGACCCCTTACTGTGCTGGGATGTTCT	1819
Db	538	GlyLysAlaCySalaAspCysCySLeuAlaArgAspProTyrCySalaTrpAspGlyAsn	557
Qy	1820	GCATGTTCTCGCTATTATTTCCCACTGCAAGAGACGACAAAGACGACAAGATATAAGAAAT	1879
Db	558	AlaCysSerArgTyrAlaProThrSerLysLysArgAlaArgGlnAspValLysTyr	577
Qy	1880	GGAGACCCACTGACTCTGCTTCCAGACTTACACCATGATATCACCATGCCACAGCCCT	1939
Db	578	GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596
Qy	1940	GAAGAGAGATCATCTATGTGTAGAGATAGTAGACATTTTGGATATCGATCCGAAG	1999
Db	597	AspGlnLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
Qy	2000	TCGCAGAGAGCGTGGTCTATTGGCAATTCAGAGGCGAAATCAAGAGCGCAAAAGAAAGAG	2059
Db	617	SerGlnGlnAlaThrIleLysTyrTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu	636
Qy	2060	ATCAGAGTGGATGATCATCATCATCAGAGACAGATCAAGCGCTTCTGCTACGTAGTCTACAA	2119
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln	656
Qy	2120	CAGAGATTTCAGCAATTACTCTGCCATCGCGTGGAAACATGGTGTCTACATAAACTCTT	2179
Db	657	LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle	676
Qy	2180	CTTAAGGTACCCCTGGAAGTCATTGACACAGACGATTTGGAAGAACTTCTTCATAAAGAT	2239
Db	677	ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu	696
Qy	2240	GATGATCGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGCACCTAGCCAGAAG	2299
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
Qy	2300	GTCGTGTACAGAGACTTCATGCGACTCATCAACCCCAATCTCAACAGATGGATGAG	2359
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln	729
Qy	2360	TTCTGTGAACAAGTTTGGAAAGGGCCGCAAAACACAGTCGCGCAAGGCCAGGCATACAC	2419
Db	730	TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgGlnAsnLysGlyGly-----	747
Qy	2420	CCAGGGAACAGTAAACAAATGGAAGCACTTACAAAGAAATTAAGAAAGGTAGAAACAGGAGG	2479
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Qy	2480	ACCCAC---GAATTTGAGAGGCCACCCAGAGTGTC	2512
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RESULT 15			
US-10-176-915-348			
; Sequence 348, Application US/10176915			
; Publication No. US20030017544A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3430R1C110			
; CURRENT APPLICATION NUMBER: US/10/176,915			
; CURRENT FILING DATE: 2002-06-21			


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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: prt
; ORGANISM: Homo sapien
US-10-176-915-348

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Alignment Scores:

Pred. No.:	2,438-201	Length:	777
Score:	2245.50	Matches:	413
Percent Similarity:	73.67%	Conservative:	141
Best Local Similarity:	54.92%	Mismatches:	177
Query Match:	45.86%	Indels:	21
DB:	14	Gaps:	9

US-09-774-490-1 (1-2709) x US-10-176-915-348 (1-777)

[illegible]

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677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db   ::::: ||| :::::
697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGGTACAGAGACTTCATGAGTCTCATCAACCCCAATCTCAACACGATGGATGAG 2359
Db   ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| :::::
711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTTGGAAAAGGACCGAAACACACGTCGGCAAGGCCAGGACATACC 2419
Db   ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: ||| ::::: |||
730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
QY 2420 CCAGGGAACAGTAACAAATGGAAGCAGCTTACAGAAATAAGAAAGGTAGAAACAGAGG 2479
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCCAC---GAATTTGAGAGGCGACCCAGGAGTGTC 2512
Db   ||| ::::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775

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Search completed: March 8, 2005, 21:39:35
Job time : 398 secs

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